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L1   0 HEIRARCHICAL AND NON-HIERARCHICAL

=> s hierarchical and non-hierarchical
L2   150 HIERARCHICAL AND NON-HIERARCHICAL

=> s l2 and clustering
L3   39 L2 AND CLUSTERING

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L4   ANSWER 1 OF 35   MEDLINE on STN
AN   2004165716   IN-PROCESS
DN   PubMed ID: 15059657
TI   Towards realistic description of collective motions in the lattice protein
      folding models.
AU   Yesylevskyy S O; Demchenko A P
CS   A.V. Palladin Institute of Biochemistry, Leontovicha Street 9, Kiev 01030,
      Ukraine.
SO   Biophysical chemistry, (2004 Apr 1) 109 (1) 17-40.
      Journal code: 0403171. ISSN: 0301-4622.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   IN-PROCESS; NONINDEXED; Priority Journals
ED   Entered STN: 20040403
      Last Updated on STN: 20040430
AB   Collective motions and the formation of clusters of residues play an
      important role in the folding of real proteins. However, existing Monte
      Carlo (MC) techniques of the protein folding simulations based on highly
      popular lattice models provide only a schematic representation of
      collective motions, which is rather far from physical reality. The

Clustering Monte Carlo (CMC) algorithm was developed with
particular aim to provide a realistic description of collective motions on
the lattice. CMC allows modeling the cluster dynamics and the effects of
the solvent viscosity, which is impossible in conventional algorithms. In
this study two 2D lattice peptides, with the ground states of
hierarchical and **non-hierarchical** design, were
investigated comparatively using three methods: Metropolis MC with the
local move set, Metropolis MC with unspecific rigid rotations and the CMC
algorithm. We present evidence that the folding pathways and kinetics of
hierarchically folding clustered sequence are not adequately described in
conventional MC simulations, and the account for cluster dynamics provided
by CMC allows to capture essential features of the folding process. Our
data suggest that the methods, which enable specific cluster motions, such
as CMC, should be used for a more realistic description of protein
folding.

L4	ANSWER 2 OF 35	MEDLINE on STN	DUPLICATE 1
AN	2003173350	MEDLINE	
DN	PubMed ID: 12691990		
TI	Client-server environment for high-performance gene expression data analysis.		
AU	Sturn Alexander; Mlecnik Bernhard; Pieler Roland; Rainer Johannes; Truskaller Thomas; Trajanoski Zlatko		
CS	Institute of Biomedical Engineering, Graz University of Technology, Christian Doppler Laboratory for Genomics and Bioinformatics, Krenngasse 37, 8010 Graz, Austria.		
SO	Bioinformatics (Oxford, England), (2003 Apr 12) 19 (6) 772-3. Journal code: 9808944. ISSN: 1367-4803.		
CY	England: United Kingdom		
DT	Journal; Article; (JOURNAL ARTICLE)		
LA	English		
FS	Priority Journals		
EM	200312		
ED	Entered STN: 20030416 Last Updated on STN: 20031217 Entered Medline: 20031216		
AB	SUMMARY: We have developed a platform independent, flexible and scalable Java environment for high-performance large-scale gene expression data analysis, which integrates various computational intensive **hierarchical** and **non-hierarchical** **clustering** algorithms. The environment includes a powerful client for data preparation and results visualization, an application server for computation and an additional administration tool. The package is available free of charge for academic and non-profit institutions.		

L4	ANSWER 3 OF 35	MEDLINE on STN	DUPLICATE 2
AN	2003519799	MEDLINE	
DN	PubMed ID: 14596807		
TI	Parameterization and classification of the protein universe via geometric techniques.		
AU	Tendulkar Ashish V; Wangikar Pramod P; Sohoni Milind A; Samant Vivekanand V; Mone Chetan Y		
CS	Kanwal Rekhi School of Information Technology, Indian Institute of Technology, Bombay, Powai, Mumbai 400 076, India.		
SO	Journal of molecular biology, (2003 Nov 14) 334 (1) 157-72. Journal code: 2985088R. ISSN: 0022-2836.		

AB We present a scheme for the classification of 3487 non-redundant protein
   structures into 1207 **non-hierarchical** clusters by
   using recurring structural patterns of three to six amino acids as keys of
   classification. This results in several signature patterns, which seem to
   decide membership of a protein in a functional category. The patterns
   provide clues to the key residues involved in functional sites as well as
   in protein-protein interaction. The discovered patterns include a
   "glutamate double bridge" of superoxide dismutase, the functional
   interface of the serine protease and inhibitor, interface of homo/hetero
   dimers, and functional sites of several enzyme families. We use geometric
   invariants to decide superimposability of structural patterns. This
   allows the parameterization of patterns and discovery of recurring
   patterns via **clustering.** The geometric invariant-based approach
   eliminates the computationally explosive step of pair-wise comparison of
   structures. The results provide a vast resource for the biologists for
   experimental validation of the proposed functional sites, and for the
   design of synthetic enzymes, inhibitors and drugs.

L4 ANSWER 4 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AB Observer-independent cytoarchitectonic mapping of the cerebral cortex(1,2)
   is based on the statistical analysis of its laminar pattern. This method
   reliably detects the position of areal borders by the identification of
   significant cytoarchitectonic changes. We here show an extension of this
   method, which enables an exploratory analysis of the laminar pattern in
   neighboring histological sections. Hereby, identical areas are identified
   automatically based on the measurement of cytoarchitectonic features. The
   GLI was measured as an indicator of the volume fraction of cell bodies.
   Profiles were obtained perpendicular to the cortical layers and their
   shape was quantified by 10 features(1). Architectonic borders were
   identified at those profiles-positions, where the multivariate Mahalanobis
   distance between neighboring groups of profiles showed local maxima(2).
   They were used to define the seeds for a **hierarchical** cluster
   analysis of the profiles within a section. A cut-off, representing the

most plausible number of groups, was calculated by evaluating a "penalty-function" based on the number of clusters and the introduced increase in variance. By applying a **non-hierarchical clustering**, the resulting classification of the profiles into areas was then used for recognizing identical areas on different sections.Results are in good accordance to those of visual inspection and established observer-independent methods(2). Our approach distinguishes reliably between cortical areas, as well as finer parcellations, e.g. within the extrastriate cortex. The approach automatically recognizes corresponding parts of the same cortical area in different sections and compensates for local variations and artifacts. This novel approach based on cluster analysis thus enables an automated, exploratory analysis of the cytoarchitecture in series of histological sections. 1 Schleicher et al,(1990) J Microsc 157:3672 Schleicher et al,(2000) J Chem Neuroanat 20:31.

AN   2001:221538 BIOSIS
DN   PREV200100221538
TI   Comparison between modern **clustering** techniques and original
      macrobenthic community classification on A. Vatova's Adriatic data set
      (1934-36).
AU   Di Dato, P. [Reprint author]; Fresi, E. [Reprint author]; Scardi, M.
CS   Dipartimento di Biologia, Universita di Roma "Tor Vergata", Via della
      Ricerca Scientifica, 00133, Roma, Italy
SO   Faranda, F. M.; Guglielmo, L.; Spezie, G. (2001) pp. 271-275.
      Mediterranean ecosystems: Structures and processes. print.
      Publisher: Springer-Verlag Italia Srl, Via Podgora 4, I-20122, Milan,
      Italy; Springer-Verlag New York Inc., 175 Fifth Avenue, New York, NY,
      10010-7858, USA.
      ISBN: 88-470-0114-5 (cloth).
DT   Book
      Book; (Book Chapter)
LA   English
ED   Entered STN: 9 May 2001
      Last Updated on STN: 18 Feb 2002

AN   2001:331507 BIOSIS
DN   PREV200100331507
TI   An avifaunal zonation of Switzerland and its relation to environmental
      conditions.
AU   Pasinelli, Gilberto; Naef-Daenzer, Beat [Reprint author]; Schmid, Hans
      [Reprint author]; Keller, Verena [Reprint author]; Holzgang, Otto [Reprint
      author]; Graf, Roman [Reprint author]; Zbinden, Niklaus [Reprint author]
CS   Swiss Ornithological Institute, 6204, Sempach, Switzerland
      gpasi@vt.edu
SO   Global Ecology and Biogeography, (May, 2001) Vol. 10, No. 3, pp. 261-274.
      print.
      ISSN: 1466-822X.
DT   Article
LA   English
ED   Entered STN: 11 Jul 2001
      Last Updated on STN: 19 Feb 2002
AB   1 We propose a quantitative zonation of Switzerland based on the
      distribution of breeding birds. We use a combined dataset from two

nationwide bird censuses 20 years apart to account for distribution changes between the censuses. This approach approximates the 'potential' distribution of species more closely than a dataset from one period only. 2 A numerical approach with correspondence analysis and **non-hierarchical clustering** resulted in five avifaunal
regions, consisting of two lowland regions north of the alpine arch, two alpine regions and one region of southern alpine valleys. 3 We identified characteristic species for each region using the indicator value analysis of Dufrene and Legendre (1997) and determined environmental conditions separating the regions with discriminant analysis. 4 Our zonation partly corresponds with previous subdivisions of Switzerland, but has the advantage of being based on a numerical approach instead of expert knowledge. 5 We discuss avifaunal and ecological differences between the regions and relate our zonation to the classical biogeographic regions of Europe. Finally, we evaluate the importance of the zonation for bird conservation.

L4 ANSWER 7 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:185184 BIOSIS
DN PREV200100185184
TI Genetic divergence in seedling trees of Persian walnut (Juglans regia L.) for various metric nut and kernel characters in Himachal Pradesh.
AU Sharma, O. C.; Sharma, S. D. [Reprint author]
CS Department of Fruit Breeding and Genetic Resources, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, H.P., 173 230, India
    fbg@yspuhf.hp.nic.in
SO Scientia Horticulturae (Amsterdam), (16 April, 2001) Vol. 88, No. 2, pp. 163-171. print.
    CODEN: SHRTAH. ISSN: 0304-4238.
DT Article
LA English
ED Entered STN: 20 Apr 2001
    Last Updated on STN: 18 Feb 2002
AB The nature and magnitude of genetic divergence was assessed using **non-hierarchical** Euclidean cluster analysis in 229
    seedling trees of Persian walnut growing naturally in four districts of Himachal Pradesh for 15 nut and kernel characters. Minimum and maximum values of coefficients of variability were recorded for nut width and kernel weight, respectively. All genotypes were grouped into 16 different clusters. The **clustering** pattern of walnut genotypes belonging to the same location revealed their distribution in more than one cluster showing non-parallelism between geographic and genetic diversity. Genotypes of clusters 5 and 8 were highly diverse from each other. Mean nut weight and kernel weight were highest in clusters 8 and 14, respectively. The highest mean kernel percentage and minimum shell thickness were observed in cluster 13. The highest mean value for fat was recorded in cluster 9 whereas cluster 3 had the maximum value of protein.

L4 ANSWER 8 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:73354 BIOSIS
DN PREV200200073354
TI Analysis of variation in tissue culture response for identification of indica rice genotypes suitable for transformation.
AU Visarada, K. B. R. S.; Kumar, C. H. M. Vijaya; Sarma, N. P. [Reprint author]

AB   Genetic variation for in vitro response of 22 elite indica rice cultivars
       along with Taipei-309, a japonica model variety for tissue culture
       studies, was investigated. Sequential growth stages of in vitro seed
       culture for example i) callus induction and regeneration ii) calli with
       green regions iii) calli with only shoots iv) calli with both roots and
       shoots v) calli with roots only and vi) plants per unit culture, were
       measured and analyzed by Duncan's multiple range test. The varieties were
       clustered into groups by taking into account all the in vitro growth stage
       parameters. **Clustering** of indica varieties by three methods
       viz., canonical analysis, joint score method and **non
       hierarchical** euclidean cluster analysis resulted in identification
       of 2,3 and 4 varieties respectively, in the same genetic cluster with
       Taipei-309. The analysis based on mean and standard deviation of joint
       scores for all the traits was shown to be superior to other two methods.
       Regeneration rather than callus induction was the limiting parameter in
       most of the varieties. The number of plants regenerated per unit culture
       and percent calli giving shoots was critical for any genotype before
       taking up transformation. The indica varieties Vibhava and Seshu were
       identified as close to Taipei-309 through genetic **clustering** and
       therefore should prove to be very suitable for transformation studies.

AB   Soil grid data were gathered from 156 points in the 30-ha Muizen forest
       (Ranst, Belgium). At each grid point, soil profiles were examined
       morphologically by augering to 120-cm depth. In the laboratory, pH(KCl)
       was determined on samples from every horizon. To allow numerical
       analyses, all the morphological attributes were given ordinal scores. The
       analysis consisted of two parts. First, the master horizons were split up
       into subtypes using Principal Components Analysis and a **non-
       hierarchical clustering** technique. This was necessary
       to overcome the problem of the anisotropy of the soil profiles, which
       makes it impossible to pool the data of all the horizons and analyse them
       together. Next, the distinguished horizon subtypes were used as input for

the continuous soil profile classification with the 'fuzzy k-means with extragrades' algorithm. Five different soil classes plus an extragrade class were distinguished. The distinguished soil classes exhibited a fair degree of spatial autocorrelation and correlated well with the Belgian Soil Map. The technique developed ensures the compatibility with national or global soil classification systems based on diagnostic horizons and properties on the one hand and the production of high-resolution soil classes for local use on the other. Furthermore, the developed technique allows reanalysis and optimisation of data from previous surveys.

L4   ANSWER 10 OF 35   MEDLINE on STN   DUPLICATE 3
AN   2001196655   MEDLINE
DN   PubMed ID: 11222259
TI   PAQ: Partition Analysis of Quasispecies.
AU   Baccam P; Thompson R J; Fedrigo O; Carpenter S; Cornette J L
CS   Department of Mathematics, Iowa State University, Ames, IA 50011, USA..
      pbaccam@lanl.gov
SO   Bioinformatics (Oxford, England), (2001 Jan) 17 (1) 16-22.
      Journal code: 9808944. ISSN: 1367-4803.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200105
ED   Entered STN: 20010517
      Last Updated on STN: 20010517
      Entered Medline: 20010510
AB   MOTIVATION: The complexities of genetic data may not be accurately
      described by any single analytical tool. Phylogenetic analysis is often
      used to study the genetic relationship among different sequences.
      Evolutionary models and assumptions are invoked to reconstruct trees that
      describe the phylogenetic relationship among sequences. Genetic databases
      are rapidly accumulating large amounts of sequences. Newly acquired
      sequences, which have not yet been characterized, may require preliminary
      genetic exploration in order to build models describing the evolutionary
      relationship among sequences. There are **clustering** techniques
      that rely less on models of evolution, and thus may provide nice
      exploratory tools for identifying genetic similarities. Some of the more
      commonly used **clustering** methods perform better when data can be
      grouped into mutually exclusive groups. Genetic data from viral
      quasispecies, which consist of closely related variants that differ by
      small changes, however, may best be partitioned by overlapping groups.
      RESULTS: We have developed an intuitive exploratory program, Partition
      Analysis of Quasispecies (PAQ), which utilizes a **non-
      hierarchical** technique to partition sequences that are genetically
      similar. PAQ was used to analyze a data set of human immunodeficiency
      virus type 1 (HIV-1) envelope sequences isolated from different regions of
      the brain and another data set consisting of the equine infectious anemia
      virus (EIAV) regulatory gene rev. Analysis of the HIV-1 data set by PAQ
      was consistent with phylogenetic analysis of the same data, and the EIAV
      rev variants were partitioned into two overlapping groups. PAQ provides
      an additional tool which can be used to glean information from genetic
      data and can be used in conjunction with other tools to study genetic
      similarities and genetic evolution of viral quasispecies.

L4   ANSWER 11 OF 35 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN   2001:279111 BIOSIS
DN   PREV200100279111
TI   Introduction to the exploration of multivariate biological data.
AU   Podani, Janos [Reprint author]
CS   L. Eotvos University, Budapest, Hungary
SO   Podani, Janos. (2000) pp. i-vi, 1-407. Introduction to the exploration of
      multivariate biological data. print.
      Publisher: Backhuys Publishers, P. O. Box 321, 2300 AH, Leiden,
      Netherlands.
      ISBN: 90-5782-067-6 (paper).
DT   Book
LA   English
ED   Entered STN: 13 Jun 2001
      Last Updated on STN: 19 Feb 2002
AB   This book collects the major aspects of applying multivariate analysis to
      general biological problems. The chapters illustrate a large diversity of
      biological topics to illuminate as many approaches to data exploration as
      possible. Selected software packages that facilitate analysis are
      discussed. The book includes bibliographical references and a subject
      index.

L4   ANSWER 12 OF 35   MEDLINE on STN
AN   2001127964   MEDLINE
DN   PubMed ID: 11097075
TI   An empirical approach to subtype identification in individuals with social
      phobia.
AU   Eng W; Heimberg R G; Coles M E; Schneier F R; Liebowitz M R
CS   Adult Anxiety Clinic, Temple University, Philadelphia, PA, USA.
NC   MH40121 (NIMH)
      MH44119 (NIMH)
      MH47831 (NIMH)
      +
SO   Psychological medicine, (2000 Nov) 30 (6) 1345-57.
      Journal code: 1254142. ISSN: 0033-2917.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200102
ED   Entered STN: 20010322
      Last Updated on STN: 20010322
      Entered Medline: 20010222
AB   BACKGROUND: The present study used cluster analysis procedures to identify
      empirically subgroups of patients with social phobia in a large clinical
      sample. METHOD: The Liebowitz Social Anxiety Scale (LSAS) was
      administered to 382 patients from several studies of the treatment of
      social phobia. LSAS fear ratings were summed into four subscale scores
      (social interaction, public speaking, observation by others, eating and
      drinking in public) based on a previous factor analytical study of the
      LSAS. In order to produce a stable and robust solution, these factor
      scores were submitted to a two-stage **clustering** procedure
      consisting of an agglomerative-**hierarchical clustering**
      method followed by an iterative **non-hierarchical
      clustering** method. RESULTS: Three patient subgroups were
      identified based on their pattern of feared social situations on the LSAS.
      These groups were labelled: (1) pervasive social anxiety; (2) moderate

social interaction anxiety; and (3) dominant public speaking anxiety. Clusters differed significantly on age and age of social phobia onset, as well as on measures of social anxiety, general anxiety and depressive symptomatology. Clusters also differed in the percentage of assigned patients who met criteria for the generalized subtype of social phobia and avoidant personality disorder. CONCLUSIONS: The results provide empirical support for the existence of three subgroups in a clinical sample of individuals with social phobia and contribute to the growing evidence for the heterogeneity of social phobia. Further study of the conceptual, clinical and aetiological significance of these subgroups is needed.

AB   1. Here we classify selected European hydrophytes into 'attribute groups'
      based on the possession of homogenous sets of characteristics, and explore
      the correspondence between these attribute groups, or individual
      attributes, and habitat use. 2. **Non-hierarchical
      clustering** was used to assign 120 species to twenty groups based
      on a matrix of categorical scores for literature- and field-derived
      information covering seventeen intrinsic morphological and life-history
      traits. Subdivision of some of these traits produced a total of 58
      attributes (i.e. modalities). The robustness of this classification was
      confirmed by a high rate of reclassification (92%) under multiple
      discriminant analysis (MDA). The phylogenetic contribution was explored
      using ordination methods with taxonomy at family level acting as a
      covariable. 3. Our approach differed from earlier classifications based
      on growth or life form because we regarded growth form plasticity as a
      property of the species and its range of growing conditions, rather than
      of each individual population, and we considered additional (e.g.
      regenerative) traits. However, some conventional life form groups were
      preserved (i.e. utricularids, isoetids, hydrocharids and lemnids). 4.
      Some parallels existed with established theory on terrestrial plant growth
      strategies, but we used strictly intrinsic attributes relevant
      specifically to hydrophytes and our groups could not be decomposed into
      three or four primary strategies. Only finer levels of partitioning
      appear to be of fundamental and applied ecological relevance in
      hydrophytes. 5. A principal components analysis ordination based on 26
      attributes related to physical habitat utilization separated species and
      their attribute groups along axes relating to: (a) flow, substratum grade
      and organic matter content, scour frequency, and sedimentation; and (b)
      depth, water level stability and biotic disturbance. A MDA applied to
      species ordination scores indicated only a modest overall correspondence
      between attribute groups and habitat use (54% correct reclassification).

Poor reclassification was the result of intergroup overlap (indicating
alternative sets of attributes for a given habitat) or high intragroup
variance in habitat utilization (indicating commonality of attributes
between different habitats). These results are interpreted in terms of
trade-offs between resistance and resilience traits, 'functional
plasticity' in traits, phylogenetic dependence in some groups and
methodological constraints. The predictive potential of hydrophyte groups
and their limitations are discussed. 6. Redundancy analysis revealed a
highly significant correlation between traits and habitat use (P < 0.01).
Our attribute matrix explained 72% of variation in physical habitat use
with eight attributes (i.e. turions, anchored emergent leaves, high or low
body flexibility, high root:shoot biomass ratio, free-floating surface or
free-floating submerged growth form, and annual life history) explaining
half of this variation. 7. Most attributes were mapped in accordance with
habitat template predictions, although tests were confounded by the
underlying correlation between spatial and temporal heterogeneity. The
main features were: (a) a trade-off between resistance-type traits
(related to stream lining, flexibility and anchorage) in more spatially
heterogenous riverine and littoral zone habitats, and resilience type
traits (i.e. turions, very small body size and free-floating growth forms)
in spatially simple, rarely disturbed habitats, such as backwaters and
canals; and (b) a shift from high investment competitive traits with a low
reproductive output in deep stable habitats to classically ruderal and
desiccation resistance traits in shallow fluctuating habitats.

L4   ANSWER 14 OF 35   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:253766 BIOSIS
DN   PREV199900253766
TI   Use of cluster analysis to validate IHS diagnostic criteria for migraine
      and tension-type headache.
AU   Bruehl, Stephen [Reprint author]; Lofland, Kenneth R.; Semenchuk,
      Elizabeth M.; Rokicki, Lori A.; Penzien, Donald B.
CS   Center for Pain Studies, Rehabilitation Institute of Chicago, 345 East
      Superior Street, Room 904, Chicago, IL, 60611, USA
SO   Headache, (March, 1999) Vol. 39, No. 3, pp. 181-189. print.
      CODEN: HEADAE. ISSN: 0017-8748.
DT   Article
LA   English
ED   Entered STN: 2 Jul 1999
      Last Updated on STN: 2 Jul 1999
AB   Cluster analysis was used to validate headache diagnostic criteria of the
      International Headache Society (IHS). Structured diagnostic interviews
      were conducted on 443 headache sufferers from a community sample, which
      was randomly split to allow replication. **Hierarchical** cluster
      analysis of symptoms in both subsamples revealed two distinct (P<.001)
      clusters: (1) unilateral pulsating pain, pain aggravated by activity, and
      photophobia and phonophobia, and (2) bilateral pressing/tightening pain,
      mild to moderate intensity, and absence of nausea/vomiting. These
      clusters were consistent with IHS migraine and tension-type
      classifications, respectively. Replication using a **non-
      hierarchical clustering** technique, k-means cluster
      analysis, revealed a migrainelike patient cluster, reflecting more
      frequent pulsating, unilateral pain; more severe pain; and pain aggravated
      by activity; nausea, vomiting, photophobia, and phonophobia. A
      tensionlike patient cluster was also identified, reflecting more frequent
      pressing/tightening pain, mild to moderate pain, bilateral location, and

absence of nausea/vomiting. These patient clusters were consistent across subsamples. International Headache Society diagnoses corresponded with classification based upon statistically derived clusters (P<.001). These results indicate that headache symptoms cluster empirically in a manner consistent with IHS criteria for migraine and tension-type headaches. Criterion overlap problems regarding pain intensity and duration were identified. Overall, these data support migraine and tension-type headache as distinct entities, and provide support for the IHS diagnostic criteria with minor modifications.

L4   ANSWER 15 OF 35   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:238053   BIOSIS
DN   PREV199900238053
TI   Classification and receptor modeling of wet precipitation data from
      Central Austria (1984-1993).
AU   Simeonov, V. [Reprint author]; Puxbaum, H.; Tsakovski, S.; Sarbu, C.;
      Kalina, M.
CS   Faculty of Chemistry, University of Sofia 'St. Kliment Okhridski', J.
      Bourchier Blvd. 1, 1126, Sofia, Bulgaria
SO   Environmetrics, (March-April, 1999) Vol. 10, No. 2, pp. 137-152. print.
      ISSN: 1180-4009.
DT   Article
LA   English
ED   Entered STN: 17 Jun 1999
      Last Updated on STN: 17 Jun 1999
AB   Various classification procedures (**hierarchical** and **non
      -hierarchical** crisp and fuzzy **clustering**,
      cross-classification fuzzy **clustering**) and principal component
      analysis (varimax rotation) combined with receptor modeling are applied to
      a data set consisting of wet deposition loads of major ions from five
      sampling sites in Central Austria collected in a period of 10 years
      (1984-1993). The data classification with respect to the sampling sites
      as objects has shown that a distinct separation between sites located at
      the northern Alpine rim (Reutte, Kufstein and Haunsberg) and in the inner
      Alpine region (Innervillgraten and Werfenweng) is achieved indicating in
      this way the role of the geographical disposition of the sampling sites.
      Both cluster and principal components analysis proved that three
      conditional (latent) factors are responsible for the data structure called
      in this study 'anthropogenic', 'crustal' and 'mixed salt' - (NH_4+, SO_42-,
      NO_3-, $H+$), (Ca_2+, Mg_2+), ($K+$, $Na+$, $Cl-$), respectively. The source
      apportioning model has indicated that anthropogenic gaseous emissions
      might be responsible for the first factor, natural crustal influences and
      Sahara events for the second and sea salt and manure for the third.

L4   ANSWER 16 OF 35   MEDLINE on STN
AN   1998178077   MEDLINE
DN   PubMed ID: 9517009
TI   An evaluation of structural descriptors and **clustering** methods
      for use in diversity selection.
AU   Brown R D; Martin Y C
CS   Pharmaceutical Products Division, Abbott Laboratories, Abbott Park, IL
      60064-350, USA.
SO   SAR and QSAR in environmental research, (1998) 8 (1-2) 23-39.
      Journal code: 9440156. ISSN: 1062-936X.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)

AB   An evaluation of the suitability of a number of structural descriptors and
      clustering methods for use in diversity selection is presented.
      The methods are compared by their success in simulated biological activity
      predictions. The results suggest that simple 2D structural descriptors
      are particularly effective and that **hierarchical
      clustering** methods are superior to the **non-
      hierarchical** methods traditionally used for diversity related
      tasks. Results are presented which suggest that the difference in the
      utility of the descriptors can be accounted for by the different extent to
      which each encodes information relevant to the forces of ligand-receptor
      binding.

AN   1998:223350 BIOSIS
DN   PREV199800223350
TI   Hybrids and phylogenetic systematics III. Comparison with distance
      methods.
AU   McDade, Lucinda A. [Reprint author]
CS   Dep. Ecol. Evolutionary Biol., Plant Sci., Univ. Arizona, Tucson, AZ
      85721, USA
SO   Systematic Botany, (Oct.-Dec., 1997) Vol. 22, No. 4, pp. 669-683. print.
      CODEN: SYBODA. ISSN: 0363-6445.
DT   Article
LA   English
ED   Entered STN: 20 May 1998
      Last Updated on STN: 20 May 1998
AB   Three distance methods including two **hierarchical
      clustering** methods (average linkage (UPGMA) and Neighbor joining,
      NJ) and one **non-hierarchical** ordination method
      (Multidimensional Scaling, MDS) were used to analyze data sets including
      taxa of known hybrid origin and their parents. Whereas goodness of fit
      measures indicated reduced success of MDS and parsimony analyses with
      increasing numbers of hybrids, neither UPGMA nor NJ analyses were affected
      by number of hybrids. Compared to analyses with the same number of taxa,
      all of which were species, goodness of fit measures indicated that all
      analytic methods had more difficulty handling species than hybrids. These
      measures are unlikely, therefore, to provide any signal of the presence of
      hybrids. Results were also compared in terms of placement of hybrids
      relative to parents and other taxa. UPGMA (and raw distance values)
      reliably placed many hybrids closest to one or both parents. In contrast,
      NJ placed hybrids in the same manner as parsimony: usually as the basal
      member of a lineage including one or both parents along with other taxa.
      These results support the idea that NJ yields topologies that are similar
      to explicit phylogenetic methods. However, in the special case of
      hybrids, these topologies, in parallel with those from parsimony analyses,
      provide no indication of the presence or special evolutionary history of
      hybrids. If identification of hybrids is the goal, these results suggest
      that pairwise distances are more useful than any of the methods explored.

TI   Vegetation on hill slopes in southern Wello, Ethiopia: Degradation and
        regeneration.
AU   Tekle, Kebrom [Reprint author]; Backeus, I.; Skoglund, J.; Woldu, Zerihun
CS   Dep. Ecological Botany, Uppsala Univ,. Villavagen 14, S-752 36 Uppsala,
        Sweden
AB   A study was made of the vegetation in southern Wello (Ethiopia) in
        relation to human impact and the environment. 65 sample plots were laid
        out and analysed with respect to the cover value of vascular plant
        species. Altitude, slope, aspect and estimates of grazing pressure for
        each plot were also recorded along with physical and chemical soil
        properties analysed for samples taken from each plot. The following
        environmental factors, isolated by forward selection, show correlation
        with the axes of Canonical Correspondence Analysis (CCA): altitude,
        grazing, pH, K, Ca, Mg, slope and aspect. Through **hierarchical**
        and **non-hierarchical clustering** methods the
        vegetation was divided into eight types, from which one was secondary
        forest characterised by patch dominance of Juniperus procera and Olea
        europaea ssp. cuspidata. These forest patches are found at high altitude
        sites and because of their inaccessibility are usually characterised by
        low livestock density and consequently low grazing pressure. The presence
        of large boulders and stones in Podocarpus falcatus forest decreases
        accessibility and creates natural protection for the trees. The other
        vegetation types. most of which are found at lower altitude and associated
        with varying intensities of grazing. include grasslands (grazed and
        protected), regenerating sites dominated by Euclea racemosa and Dodonaea
        angustifolia. dense and open shrublands and Olea europaea ssp. cuspidata
        woodlands. Human interference has a major impact on the vegetation of the
        study area and its recovery will depend on the degree of participation of
        the local people.

TI   The analysis of large scale data taken from the world groundnut (Arachis
        hypogaea L.) germplasm collection: I. Two-way quantitative data.
AU   Harch, B. D. [Reprint author]; Basford, K. E.; Delacy, I. H.; Lawrence, P.
        K.
CS   CSIRO, Math. Inf. Sci., PMB 2, Glen Osmond, SA 5064, Australia
AB   Data associated with germplasm collections are typically large and
        multivariate with a considerable number of descriptors measured on each of
        many accessions. Pattern analysis methods of **clustering** and
        ordination have been identified as techniques for statistically evaluating

the available diversity in germplasm data. While used in many studies, the approaches have not dealt explicitly with the computational consequences of large data sets (i.e. greater than 5000 accessions). To consider the application of these techniques to germplasm evaluation data, 11328 accessions of groundnut (Arachis hypogaea L) from the International Research Institute for the Semi-Arid Tropics, Andhra Pradesh, India were examined. Data for nine quantitative descriptors measured in the rainy and post-rainy growing seasons were used. The ordination technique of principal component analysis was used to reduce the dimensionality of the germplasm data. The identification of phenotypically similar groups of accessions within large scale data via the computationally intensive **hierarchical clustering** techniques was not feasible and **non-hierarchical** techniques had to be used. Finite mixture models that maximise the likelihood of an accession belonging to a cluster were used to cluster the accessions in this collection. The patterns of response for the different growing seasons were found to be highly correlated. However, in relating the results to passport and other characterisation and evaluation descriptors, the observed patterns did not appear to be related to taxonomy or any other well known characteristics of groundnut.

L4 ANSWER 20 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:198429 BIOSIS
DN PREV199799497632
TI Evaluation of genetic divergence in wheat (Triticum aestivum L.) germplasm.
AU Walia, D. P. [Reprint author]; Garg, D. K.
CS Dep. Fruit Breeding, Univ. Horticulture Forestry, Nauni, Solan 173 230, India
SO Indian Journal of Genetics and Plant Breeding, (1996) Vol. 56, No. 4, pp. 452-457.
    CODEN: IJGBAG. ISSN: 0019-5200.
DT Article
LA English
ED Entered STN: 12 May 1997
    Last Updated on STN: 12 May 1997
AB The nature and magnitude of genetic diversity was assessed using **non-hierarchical** euclidean cluster analysis in 405 pure breeding lines of T. aestivum for grain yield and its associated traits. All the genotypes got grouped in 13 different clusters. The **clustering** pattern of the genotypes belonging to the same country revealed their distribution in more than one cluster showing nonparallelism between geographic and genetic diversity. Members of cluster IV and IX were highly diverse from each other. Cluster VI had high mean values for grain yield, biological yield, number of tillers/unit area and harvest index. A number of genotypes were also identified which may serve as potent genetic donors for some metric traits.

L4 ANSWER 21 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1996:573845 BIOSIS
DN PREV199799288526
TI Floristic patterns and phytogeography of Skane, S Sweden.
AU Andersson, Per-Arne [Reprint author]; Weimarck, Gunnar
CS Dep. Ecological Botany, Villavagen 14, S-752 36 Uppsala, Sweden
SO Acta Universitatis Upsaliensis Symbolae Botanicae Upsalienses, (1996) Vol. 31, No. 3, pp. 239-264.

DT   Article

LA   English

ED   Entered STN: 23 Dec 1996
Last Updated on STN: 23 Dec 1996

AB   Dot maps of the distribution of 895 vascular plant taxa in the province of
Skane, S Sweden, were digitized and the records assigned to 483 quadrats
of 5 times 5 km each. Quadrats and species were classified by the
non-hierarchical agglomerative **clustering**
program TABORD and ordinated by the program DECORANA. The results are
given in a phytosociological table and as grid map plots and ordination
graphs. Gradients are interpreted and clusters described in terms of
Ellenberg's indicator scores. A regional floristic subdivision of the
province in eight areas is proposed. The position of the border, 'limes
scanicus', between two previously proposed major areas is modified here.

L4   ANSWER 22 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN   1996:43753 BIOSIS

DN   PREV199698615888

TI   Ecological Computations Series, Volume 6. Multivariate data analysis in
ecology and systematics: A methodological guide to the SYN-TAX 5.0
package.

AU   Podani, Janos

CS   Dep. Plant Ecol. Taxon., L. Eotvos Univ., Ludovika ter 2, H-1083 Budapest,
Hungary

SO   Podani, J. (1994) pp. 316p. Ecological Computations Series; Multivariate
data analysis in ecology and systematics: A methodological guide to the
SYN-TAX 5.0 package.
Publisher: SPB Academic Publishing bv, PO Box 97747, 2509 GC Amsterdam,
Netherlands. Series: Ecological Computations Series.
ISBN: 90-5103-094-0.

DT   Book
Software Review

LA   English

ED   Entered STN: 2 Feb 1996
Last Updated on STN: 2 Feb 1996

AB   This book is a guide to the SYN-TAX 5.0 programs. SYN-TAX 5.0 is a
package of over 50 programs designed for multivariate statistical analyses
in ecological and statistical studies. The programs operate under DOS and
may be initiated from Windows. The book describes the use of SYN-TAX in
non-hierarchical and **hierarchical**
clustering, ordination and matrix rearrangement, comparisons,
consensus techniques, Mote Carlo simulations, and analysis of multispecies
point patterns. A glossary, references, and a subject index are included,
and the text is illustrated with graphs, charts, mathematical formulae,
and tables.

L4   ANSWER 23 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN   1994:526576 BIOSIS

DN   PREV199497539576

TI   Computer-assisted mapping of paddy-field soils: II. Classification,
mapping and significance.

AU   Ishida, Tomoyuki [Reprint author]; Ando, Ho

CS   Fac. Agric., Kagawa Univ., Kida-gun, Kagawa 761-07, Japan

SO   Soil Science and Plant Nutrition, (1994) Vol. 40, No. 3, pp. 403-414.
CODEN: SSPNAW. ISSN: 0038-0768.

AB   In order to determine how a conventional soil map on a local scale can be
     reproduced from soil sample information, a set of numerical procedures was
     applied to the soil chemical data from 159 soil samples collected in paddy
     fields of the Aizu Basin, in the northern part of Japan. The digital
     elevation data were also included as an attribute. Various steps were
     involved. In the first step, the sparse data were converted into a
     closely spaced data set. This first step was previously described in Part
     I of this paper. In the second step a multivariate ordination (principal
     component analysis) was applied to the sampling data in order to avoid
     redundancy of information. Large contributions to the first component
     were derived from the values of CEC and exchangeable Ca and Mg. In the
     third step the sampling sites were numerically classified using the
     results of four or five components obtained in the second step. A
     hierarchical clustering method was applied to provide
     the initial set of clusters for **non-hierarchical
     clustering.** In the fourth step the closely spaced data collected
     in the first step were allocated to an appropriate class obtained by using
     the **non-hierarchical clustering** method
     applied in the third step. For the allocation method, the geographic
     location of the sampling sites was included as an additional
     characteristic of the data. In the regional partition map based on the
     numerical procedures, each soil group corresponded to a soil series in the
     original conventional soil map which depended predominantly on detailed
     morphological and topographical differences. In addition, the regional
     partition map was found to provide useful information for the
     identification of factors closely related to soil fertility, by
     statistically examining the differences in rice yield among the soil
     groups.

AB   We compare three common types of **clustering** algorithms for use
     with community data. TWINSPAN is divisive **hierarchical,**
     flexible-UPGMA is agglomerative and **hierarchical,** and ALOC is
     non-hierarchical. A balanced design six-factor model
     was used to generate 480 data sets of known characteristics. Recovery of
     the embedded clusters suggests that both flexible UPGMA and ALOC are
     significantly better than TWINSPAN. No significant difference existed
     between flexible UPGMA and ALOC.

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AN    1992:522932  BIOSIS
DN    PREV199294131007; BA94:131007
TI    DIFFERENTIATION AND GROUPING CHARACTERISTICS OF VARIETAL GRAPE MUSTS AND
      WINES FROM MAJORCAN ORIGIN.
AU    MULET A [Reprint author]; BERNA A; FORCEN M
CS    DEP FOOD TECHNOL, UNIV POLITECNICA VALENCIA, CAMINO VERA 14, 46071
      VALENCIA, SPAIN
SO    American Journal of Enology and Viticulture, (1992) Vol. 43, No. 3, pp.
      221-226.
      CODEN: AJEVAC. ISSN: 0002-9254.
DT    Article
FS    BA
LA    ENGLISH
ED    Entered STN: 19 Nov 1992
      Last Updated on STN: 20 Nov 1992
AB    Forty-six samples of three Majorcan red grape musts, Manto Negro, Callet,
      and Fogoneu, from two close viticultural regions, Zona Alta and Zona Baja,
      were tested on the basis of twelve conventional variables.
      Physicochemical data were treated by pattern recognition techniques by
      means of discriminant analysis and non-hierarchical
      clustering, thus allowing characterization according to the
      geographical and varietal origin of samples.  Discriminant analysis gave
      rise to coincident classification results (average percentage error 18.5%)
      when distinguishing both varieties and zones.  Clustering
      analysis revealed a strong varietal affinity among the studied grape
      samples.  A further comparative study for the musts considered and the
      corresponding wines, previously studied for sixteen conventional
      variables, showed that in the discriminant statistical treatment
      correlation could be established among cultivars in terms of color
      intensity and nitrogen content.  Musts and wines from different zones were
      fairly related to some geographical characteristics of the regions.  When
      considering hierarchical clustering, an evident
      relationship between musts and wines was exclusively achieved by means of
      the varietal origin of the samples.

L4    ANSWER 26 OF 35     MEDLINE on STN
AN    94084457     MEDLINE
DN    PubMed ID: 1341650
TI    Cluster analysis and related techniques in medical research.
AU    McLachlan G J
CS    Department of Mathematics, University of Queensland, Australia.
SO    Statistical methods in medical research, (1992) 1 (1) 27-48.  Ref: 54
      Journal code: 9212457. ISSN: 0962-2802.
CY    ENGLAND: United Kingdom
DT    Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, ACADEMIC)
LA    English
FS    Priority Journals
EM    199401
ED    Entered STN: 19940209
      Last Updated on STN: 19990129
      Entered Medline: 19940127
AB    In this paper we review methods of cluster analysis in the context of
      classifying patients on the basis of clinical and/or laboratory type
      observations.  Both hierarchical and non-
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hierarchical methods of **clustering** are considered,
although the emphasis is on the latter type, with particular attention
devoted to the mixture likelihood-based approach. For the purposes of
dividing a given data set into g clusters, this approach fits a mixture
model of g components, using the method of maximum likelihood. It thus
provides a sound statistical basis for **clustering.** The
important but difficult question of how many clusters are there in the
data can be addressed within the framework of standard statistical theory,
although theoretical and computational difficulties still remain. Two
case studies, involving the cluster analysis of some haemophilia and
diabetes data respectively, are reported to demonstrate the mixture
likelihood-based approach to **clustering.**

L4   ANSWER 27 OF 35 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1989:355631 BIOSIS
DN   PREV198988047745; BA88:47745
TI   MIDWATER FOOD WEB IN THE VICINITY OF A MARGINAL ICE ZONE IN THE WESTERN
      WEDDELL SEA ANTARCTIC.
AU   HOPKINS T L [Reprint author]; TORRES J J
CS   DEP MARINE SCI, UNIV SOUTH FLORIDA, 140 7TH AVE SOUTH, ST PETERSBURG, FLA
      33701, USA
SO   Deep-Sea Research Part A Oceanographic Research Papers, (1989) Vol. 36,
      No. 4, pp. 543-560.
      CODEN: DRPPD5. ISSN: 0198-0149.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 2 Aug 1989
      Last Updated on STN: 2 Aug 1989
AB   The structure of the food web in the vicinity of a marginal ice zone was
      investigated in the western Weddell Sea during austral autumn 1986. The
      diets of 40 species of zooplankton and micronekton occurring in the
      epipelagic zone were examined and compared using **non-**
      hierarchical clustering procedures. Over half the
      species were in three clusters of predominately small-particle
      (phytoplankton; protozoans) grazers. These included biomass dominants
      Calanoides acutus, Calanus propinquus, Metridia gerlachei and Salpa
      thompsoni. Six clusters contained omnivores that had diets consisting of
      small particles as well as a substantial fraction of metazoan food. Among
      these was Euphausia superba. Seven groups were carnivorous, including
      species of copepods (1), chaetognaths (3), and fishes (5). Copepods were
      the most frequent food of carnivores; however krill also were important in
      the diets of three fish species. Among small-particle grazers,
      phytoplankton occurred more frequently in guts in individuals from open
      water; carnivory was more in evidence in samples collected under the pack
      ice. Regional comparisons of material taken on this and several previous
      cruises indicate that, in most of the dominant species, diets remain
      relatively consistent with respect to major food categories. Seasonal
      impact on feeding dynamics appears to be great: the guts of grazing
      species were generally much more full (visual evidence) during summer
      bloom conditions than during the autumn. The following trophic sequence
      is suggested for grazing zooplankton species in ice-covered regions of the
      Antarctic: (1) Active small-particle grazing during the summer bloom
      period; (2) reduced ingestion rates in autumn as primary production
      declines and the system becomes more oligotrophic, with some species
      augmenting grazing with carnivory; (3) descent of zooplankton biomass

species into the mesopelagic zone in late autumn-early winter with feeding largely terminated. The sequence applies to the dominant zooplankton biomass species. Feeding dynamics and vertical distribution of several of the important larger sized grazing species, such as Euphausia superba and Salpa thompsoni, remain largely unknown.

AB   Cluster analysis was applied in grouping soils based on their scores of
      the factors controlling soil variation in a cultivated, field at the
      Experimental Farm of the International Institue of Tropical Agriculture in
      Ibadan, Nigeria. The procedure employed here consisted of two steps: 1)
      grouping of the samples into a given number of provisional clusters
      through **non-hierarchical** cluster analysis, and 2)
      analysis of the similarity among those clusters using their means with
      hierarchical cluster analysis and determination of the proper
      number of the final clusters. Two initial settings in the assignment of
      the number of the provisional clusters were tested in **non-
      hierarchical** cluster analysis. Both trials gave a consistent
      classification, which also agreed with that based only on
      hierarchical cluster analysis. This combination of **non-
      hierarchical** and **hierarchical** cluster analsyses enabled
      us to pressure a soil map solely based on the factors controlling soil
      variation in the study area without introducing an a priori idea of soil
      classification. This method is not only an alternative to
      hierarchical clustering, but a more efficient tool in
      terms of capacity and computational speed to classify large numbers of
      samples which **hierarchical** cluster analysis is unable to handle.

AB   This paper presents the findings of a specifically geographical
     investigation of the incidence, distribution and social/environmental
     correlates of mental disorder in Nottingham. Three diagnostic groups were
     examined, namely schizophrenia and paranoia, the effective psychoses (or
     manic depression) and the non-psychotic mental disorders. Analysis of two
     distinct cohorts of first contact patients for both the schizophrenia and
     affective psychoses diagnoses yielded markedly dissimilar incidence rates.
     It is therefore suggested that observed variations in the incidence of
     specific mental disorders between cities probably reflect such nosocomial
     (i.e. service related) factors as diagnostic accuracy and the levels of
     local psychiatric services. It is therefore dangerous to ascribe the
     variations solely to the contrasting social/environmental milieux found in
     these cities. The spatial distributions of the selected mental disorders
     within Nottingham were analysed in the context of a set of 12 distinct
     ecological areas. These areas were derived from a matrix comprising 105
     sub-areas and 40 variables via principal components analysis and a
     non-hierarchical clustering algorithm. Marked
     spatial variation in the incidence of all the mental disorders was
     demonstrated via both traditional mapping and probability mapping
     techniques. Pearson product-moment analysis revealed that the
     distributions of the two diagnostically distinct schizophrenia and
     affective psychoses cohorts were virtually identical. The relationships
     between the inception rates for the mental disorders and
     social/environmental attributes were analysed. Stepwise multiple
     regression models for both the principal components and the individual
     census variables revealed strong and systematic relationships with all the
     mental disorders. Although such ecological analysis has limited
     explanatory power it nevertheless provides useful insights into mental
     disorder-environmental relationships. It is argued that these can be
     subsequently best examined at a disaggregated (i.e. behavioural) level.

L4   ANSWER 30 OF 35   MEDLINE on STN   DUPLICATE 4
AN   86018819   MEDLINE
DN   PubMed ID: 4048928
TI   Heterotrophic bacteria in water distribution systems. I. Spatial and
     temporal variation.
AU   Maul A; el-Shaarawi A H; Block J C
SO   Science of the total environment, (1985 Sep) 44 (3) 201-14.
     Journal code: 0330500. ISSN: 0048-9697.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   198511
ED   Entered STN: 19900321
     Last Updated on STN: 19900321
     Entered Medline: 19851114
AB   The drinking water distribution system of the city of Metz in France was
     sampled intensively during six, monthly surveys which were designed to
     determine the spatial and temporal distribution of total heterotrophic
     bacteria in the network. A **non-hierarchical**
     nearest-centroid **clustering** method was used for dividing the
     water distribution system into zones corresponding to different levels of
     bacterial density. The general pattern of the spatial heterogeneity
     showed a high degree of reproducibility. Since the frequency distribution
     of total heterotrophic bacteria within the zones was compatible with the

negative binomial distribution, the water distribution system studied may
be considered as being composed of several heterogeneous subsystems. The
consistency of this structured spatial dispersion pattern of bacteria in
light of some physical and chemical characteristics of the system is
evident. In consideration of the principal features of flow in the system
relevant to the layout of water mains, the location of zones of highest
bacterial concentrations have been attributed to lower levels of chlorine
residuals and prolonged retention time of the water in the network,
especially in the storage units, before reaching the various distribution
areas. Although the monthly variation in the bacterial concentration of
the entire system showed a marked increase which was concomitant with
warmest water temperatures, the zones were subject to noticeable
discrepancies in the range of temporal variation.

AB   A **non**-**hierarchical** nearest-centroid **clustering**
      method was used to separate data pairs consisting of the dissolved oxygen
      (DO) concentration and temperature into 4 groups corresponding to
      hypolimnetic and non-hypolimnetic water of the Central and Eastern Basins
      of Lake Erie. For the stations which were common to all cruises within a
      year and were classified as being in the hypolimnion, initial DO
      concentrations and depletion rates were calculated and tests about their
      constancy were performed using weighted regression analysis and regression
      models with the time structure of the data explicitly incoporated in the
      models. The yearly uncorrected depletion rates for 1967-1980 were similar
      to values previously reported by several authors, indicating that this
      semi-objective **clustering** procedure provides a practical
      alternative to subjective selection of data. The conclusions about
      constancy of initial concentraitons and depletion rates based on an
      unweighted regression analysis were shown to differ from those of weighted
      regression. Using regression with empirical weights, neither the initial
      DO concentration nor the depletion rate remained constant between 1967 and
      1980 in the Central Basin but the depletion rate remained constant and the
      initial DO concentration varied in the Eastern Basin.

AB   The application of **hierarchical** classification to ecological
      community data is examined, using a variety of classification techniques
      and test data sets. Problems discussed include the choice of a conceptual
      space in which points representing samples or species or both are located;
      the effects of random noise and nonlinearity; the degree to which clusters
      are natural to a data set or are imposed by the **clustering**
      technique; the choice of criteria for locating divisions;
      clustering strategies (**non-hierarchical** vs.
      hierarchical, divisive vs. agglomerative and polythetic vs.
      monothetic); the presentation of results of various **clustering**
      techniques; and methods for evaluating and comparing **clustering**
      techniques and their results. Five **hierarchical**
      clustering techniques are compared: complete linkage
      clustering, the unweighted pair group method using arithmetic
      averages, minimization of within-group dispersion, 2-way indicator species
      analysis, and partitioning of an ordination space (using detrended
      correspondence analysis, a modification of reciprocal averaging). The
      first 3 techniques are agglomerative and the last 2 are divisive. Data
      sets for tests include simulated data sets in 1 to 4 dimensions (some
      incorporating noise of 3 kinds), and field data varying in number of
      samples, noise level and number and length of community gradients.
      Two-way indicator species analysis is usually the best, but there are
      cases in which other techniques may be complementary or superior.
      Theoretical requirements and test results are discussed to show why
      clustering of ecological community data is usually best approached
      by a divisive strategy. This conclusion is important because the analysis
      may be stopped after a limited number of divisions, thus needing less
      computation than do agglomerative strategies. The 2 divisive techniques
      discussed here have computer requirements which rise only linearly with
      the amount of data, making analysis of large data sets practical.

L4   ANSWER 33 OF 35 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AB   The distributional relations of aquatic macrophytes were examined by
      correlation analysis and floristically homogeneous areas were delimited by
      multivariate principal component analysis and **non-
      hierarchical** agglomerative multivariate **clustering**
      (grouping) techniques, using data on the presence/absence and a buandance
      of the species. Species having the same or opposite distribution patterns
      and species that were evenly distributed throughout the waters were easly
      distinguished. Particular vegetationally homogeneous areas could be
      distinguished. The results remained largely the same when the data were
      treated differently or restricted. The data on the species' abundance
      make no important difference to the results yielded by the
      presence/absence data. The homogeneous areas delimited according to the

floristic similarities largely agreed with the areas distinguished on the basis of the environmental conditions, mainly water properties. The vegetation of the homogeneous areas was examined with respect to the occurrence of the life-forms and of categories of species indicate of the water quality. The results yield by the mathematical techniques agree well with those reached by convetional methods, **clustering** procedures are suitable for this kind of study, but complicated mathematical methods are not essential of reaching correct results. Average accurancy and reliability can be attained with only a selected fraction of the total vegetational data and general trends can be revealed using only a few indicator species.

AB   Depth and depth-related processes appear to exert primary control over the distributional patterns of species of polychaetous annelids in the western Beaufort Sea (Cape Halkett-Barter Island, Alaska). Species richness and total polychaete abundance are maximal along the outer continental shelf and upper continental slope. Stations exhibiting the most similar polychaete assemblages are located at similar depths. Some species distributions appear to correlate better with sediment type than with depth. Maximum abundance occurs deeper on the continental slope to the west; and station clusters generated by **non-hierarchical clustering** (using the dominant polychaete species data) are not sorted strictly by depth. In a canonical analysis of discriminance, the station clusters were projected onto a 2 dimensional plane in species space. The 1st and 2nd canonical variables of the station clusters correlate with sediment grain-size distributions, suggesting a relationship between polychaete distribution patterns and the sedimentary environment. This relationship is further substantiated when sediment grain-size distributions for each station are plotted on a tertiary diagram: the stations are grouped and ordered in a pattern similar to that generated by the canonical analysis of discriminance.

AB   The Royal Botanic Gardens Annexe at Cranbourne [Victoria, Australia]
      supports 200 ha of closed-heath, closed-scrub and low closed-forest (sensu
      Specht, 1970). Variation of the floristic composition of the vegetation
      is mostly continuous along topographic and edaphic gradients, but sharp
      discontinuities occur where permanent water is at, or close to, the soil
      surface. Studies made of regeneration after clearing suggests that if the
      topsoil is not removed floristic regeneration is complete within 8 yr,
      while structural regeneration may take up to 30 yr. A method for sorting
      2-way tables for vegetation description is included. This method employs
      a polythetic, agglomerative, **non-hierarchical
      clustering** procedure, with a data editing facility.

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS   SINCE FILE   TOTAL
                                                    ENTRY   SESSION
FULL ESTIMATED COST   58.64   58.85

STN INTERNATIONAL LOGOFF AT 09:17:25 ON 24 MAY 2004

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Welcome to STN International! Enter x:x

LOGINID:SSSPTA1805JXB

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

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                   and searchable
NEWS 4   JAN 27   A new search aid, the Company Name Thesaurus, available in
                   CA/CAplus
NEWS 5   FEB 05   German (DE) application and patent publication number format
                   changes
NEWS 6   MAR 03   MEDLINE and LMEDLINE reloaded
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NEWS 8   MAR 03   FRANCEPAT now available on STN
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NEWS 12   APR 26   PROMT: New display field available
NEWS 13   APR 26   IFIPAT/IFIUDB/IFICDB: New super search and display field
                   available
NEWS 14   APR 26   LITALERT now available on STN
NEWS 15   APR 27   NLDB: New search and display fields available
NEWS 16   May 10   PROUSDDR now available on STN
NEWS 17   May 19   PROUSDDR: One FREE connect hour, per account, in both May
                   and June 2004
NEWS 18   May 12   EXTEND option available in structure searching
NEWS 19   May 12   Polymer links for the POLYLINK command completed in REGISTRY
NEWS 20   May 17   FRFULL now available on STN

NEWS EXPRESS   MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT
               MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
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NEWS INTER   General Internet Information
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FILE 'HOME' ENTERED AT 10:28:21 ON 24 MAY 2004


=> file .pub
COST IN U.S. DOLLARS                              SINCE FILE      TOTAL
                                                    ENTRY        SESSION
FULL ESTIMATED COST                                  0.21         0.21


FILE 'MEDLINE' ENTERED AT 10:28:30 ON 24 MAY 2004


FILE 'BIOSIS' ENTERED AT 10:28:30 ON 24 MAY 2004
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=> e skierczynski/au
E1          2       SKIERCZYNSKA A/AU
E2          9       SKIERCZYNSKA J/AU
E3          0 --> SKIERCZYNSKI/AU
E4          1       SKIERCZYNSKI B/AU
E5         22       SKIERCZYNSKI B A/AU
E6          2       SKIERCZYNSKI BOGUSLAW A/AU
E7          2       SKIERCZYNSKI PAUL/AU
E8          2       SKIERCZYNSKI PAUL A/AU
E9          1       SKIERDE S/AU
E10         1       SKIERKA R L/AU
E11         2       SKIERKOWSKA B/AU
E12         2       SKIERKOWSKI J/AU


=> s e4-e6
L1         25 ("SKIERCZYNSKI B"/AU OR "SKIERCZYNSKI B A"/AU OR "SKIERCZYNSKI
              BOGUSLAW A"/AU)


=> s l1 and clustering
L2          0 L1 AND CLUSTERING


=> s l1 and hierarchical
L3          0 L1 AND HIERARCHICAL


=> e schork/au
E13         3       SCHORIN MARSHALL/AU
E14         4       SCHORIN MARSHALL A/AU
E15         0 --> SCHORK/AU
E16        91       SCHORK A/AU
E17         5       SCHORK A M/AU
E18         2       SCHORK A R/AU
E19        13       SCHORK ANTHONY/AU
E20         2       SCHORK ANTHONY M/AU
E21         1       SCHORK ANTONY/AU
E22         2       SCHORK ASTRID/AU
E23         2       SCHORK C M/AU
E24         1       SCHORK CATHERINE M/AU
```

```
=> e schork n j/au
E25        '  53      SCHORK N/AU
E26           1       SCHORK N A/AU
E27         190 -->   SCHORK N J/AU
E28           1       SCHORK N M/AU
E29           6       SCHORK NICHOLAS/AU
E30           1       SCHORK NICHOLAS A/AU
E31         100       SCHORK NICHOLAS J/AU
E32           8       SCHORK P/AU
E33           5       SCHORK P K/AU
E34           1       SCHORK S/AU
E35           3       SCHORK S M/AU
E36           2       SCHORK STEFAN M/AU

=> s e27, ee29, e31
L4          190 E27, EE29, E31

=> s l4 and hierarchical
L5            0 L4 AND HIERARCHICAL

=>

---Logging off of STN---



=>
Executing the logoff script...


=> LOG Y

COST IN U.S. DOLLARS                    SINCE FILE      TOTAL
                                          ENTRY        SESSION
FULL ESTIMATED COST                        3.69          3.90

STN INTERNATIONAL LOGOFF AT 10:31:34 ON 24 MAY 2004
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=> file .pub
COST IN U.S. DOLLARS   SINCE FILE   TOTAL
                                                    ENTRY   SESSION
FULL ESTIMATED COST   0.21   0.21

FILE 'MEDLINE' ENTERED AT 10:33:43 ON 24 MAY 2004

FILE 'BIOSIS' ENTERED AT 10:33:43 ON 24 MAY 2004
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=> s hierarchical and non-hierarchical
L1   150 HIERARCHICAL AND NON-HIERARCHICAL

=> s l1 and cluster
L2   50 L1 AND CLUSTER

=> s hierarchical and "non-hierarchical"
L3   150 HIERARCHICAL AND "NON-HIERARCHICAL"

=> s l3 and cluster
L4   50 L3 AND CLUSTER

=> duplicate remove l4
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L4
L5   48 DUPLICATE REMOVE L4 (2 DUPLICATES REMOVED)

=> s l5 and py<2000
L6   33 L5 AND PY<2000

=> d 1-33 bib ab

L6   ANSWER 1 OF 33   MEDLINE on STN
AN   1998178077   MEDLINE
DN   PubMed ID: 9517009
TI   An evaluation of structural descriptors and clustering methods for use in
      diversity selection.
AU   Brown R D; Martin Y C
CS   Pharmaceutical Products Division, Abbott Laboratories, Abbott Park, IL
      60064-350, USA.
SO   SAR and QSAR in environmental research, **(1998)** 8 (1-2) 23-39.
      Journal code: 9440156. ISSN: 1062-936X.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199804

AB   An evaluation of the suitability of a number of structural descriptors and
     clustering methods for use in diversity selection is presented. The
     methods are compared by their success in simulated biological activity
     predictions. The results suggest that simple 2D structural descriptors
     are particularly effective and that **hierarchical** clustering
     methods are superior to the **non-hierarchical** methods
     traditionally used for diversity related tasks. Results are presented
     which suggest that the difference in the utility of the descriptors can be
     accounted for by the different extent to which each encodes information
     relevant to the forces of ligand-receptor binding.

L6   ANSWER 2 OF 33   MEDLINE on STN
AN   94084457   MEDLINE
DN   PubMed ID: 1341650
TI   **Cluster** analysis and related techniques in medical research.
AU   McLachlan G J
CS   Department of Mathematics, University of Queensland, Australia.
SO   Statistical methods in medical research, **(1992)** 1 (1) 27-48.
     Ref: 54
     Journal code: 9212457. ISSN: 0962-2802.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199401
ED   Entered STN: 19940209
     Last Updated on STN: 19990129
     Entered Medline: 19940127
AB   In this paper we review methods of **cluster** analysis in the
     context of classifying patients on the basis of clinical and/or laboratory
     type observations. Both **hierarchical** and **non-**
     hierarchical methods of clustering are considered, although the
     emphasis is on the latter type, with particular attention devoted to the
     mixture likelihood-based approach. For the purposes of dividing a given
     data set into g **clusters**, this approach fits a mixture model of
     g components, using the method of maximum likelihood. It thus provides a
     sound statistical basis for clustering. The important but difficult
     question of how many **clusters** are there in the data can be
     addressed within the framework of standard statistical theory, although
     theoretical and computational difficulties still remain. Two case
     studies, involving the **cluster** analysis of some haemophilia and
     diabetes data respectively, are reported to demonstrate the mixture
     likelihood-based approach to clustering.

L6   ANSWER 3 OF 33   MEDLINE on STN
AN   89249858   MEDLINE
DN   PubMed ID: 2720980
TI   Statistical interpretation of concentrations of magnesium, zinc, calcium,
     potassium, cholesterols, and creatine kinase isoenzymes in men at
     different stages of ischemic heart disease.
AU   Speich M; Auget J L; Arnaud P

AB   We present a statistical interpretation of plasma (Pl) and (or) erythrocyte (Erc) concentrations of magnesium, zinc, calcium, potassium, and total high-density lipoprotein (HDL) cholesterol, as well as of the activity of total creatine kinase (CK) and its CK-MB isoenzyme, in 26 men with pre-infarction syndrome (PIS) and 34 men with acute myocardial infarction (MI). Discriminant analysis allowed overall comparison of both groups and determination of the most significant variables: CK and Pl-Zn. By **non-hierarchical cluster** analysis we defined three homogeneous subgroups among MI men, with CK, CK-MB, and Pl-Zn differing significantly between the groups. In PIS men, Pl-Zn was correlated with Pl-Ca, whereas in MI men Pl-Zn was correlated with Pl-Mg. Stepwise regression indicated that Pl-Zn was the most significant regressor of CK in PIS men and of CK-MB in MI men. All these statistical interpretations support a special role of Pl-Zn in diagnosis and perhaps prognosis. After MI, interleukin-1 release may possibly mediate observed hypozincemia via formation of a heart Zn-metallothionein.

AB   In the present investigation 200 genotypes of wheat (Triticum aestivum) have been grouped into sixteen **clusters** using Mahalanobis D2 statsitics, based on eight morphological characters namely; days to flowering, tiller number, plant height, 1000-grain weight, grains/ear, biological yield and harvest index. The genetic divergence was independent of pedigree as well as place of origin/place of release. Grain yield and tiller number were major contributors towards genetics divergence with moderate contribution from 1000-grain weight, grains/ear and harvest index. Grain yield was significantly and positively correlated with the component traits except plant height and days to flowering. Non-hierarchial Euclidean **cluster** analysis was also used to group 200 genotype into different number of **clusters** ranging from 2-16. Out of varying number of **clusters** (2 to 16),

the one with 10-**clusters** was taken as no major differences
either in mean cv values or their range were observed which suggested that
grouping 200 genotypes into 10-**clusters** was as effective as that
of 16-**clusters** without any loss of information.

L6   ANSWER 5 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:480550 BIOSIS
DN   PREV199900480550
TI   Eco-geographical diversity vis-a-vis agromorphological divergence in
       germplasm of forage maize (Zea mays L.).
AU   Katiyar, P. K. [Reprint author]; Choubey, R. N. [Reprint author];
       Chaudhary, B. S. [Reprint author]
CS   Indian Grassland and Fodder Research Institute, Jhansi, 284 003, India
SO   Crop Improvement, (Dec., 1998) Vol. 25, No. 2, pp. 191-196. print.
       ISSN: 0256-0933.
DT   Article
LA   English
ED   Entered STN: 16 Nov 1999
       Last Updated on STN: 16 Nov 1999
AB   Three hundred genotypes of fodder types in maize (Zea mays L.) of diverse
       eco-geographical origin were evaluated for genetic variability. Principal
       component and **non-hierarchical** Euclidean
       cluster analysis was used to compare the genotypes. Accessions
       were classified into 12 broad groups. Group E was the largest consisting
       of 35 accessions, while minimum number (18 accessions) was observed in
       cluster J. There was no parallelism between genetic and
       geographical diversity. The hybridization programme based on such
       analysis has been suggested which is likely to prove fruitful in fodder
       maize improvement programme.

L6   ANSWER 6 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:253766 BIOSIS
DN   PREV199900253766
TI   Use of **cluster** analysis to validate IHS diagnostic criteria for
       migraine and tension-type headache.
AU   Bruehl, Stephen [Reprint author]; Lofland, Kenneth R.; Semenchuk,
       Elizabeth M.; Rokicki, Lori A.; Penzien, Donald B.
CS   Center for Pain Studies, Rehabilitation Institute of Chicago, 345 East
       Superior Street, Room 904, Chicago, IL, 60611, USA
SO   Headache, (March, 1999) Vol. 39, No. 3, pp. 181-189. print.
       CODEN: HEADAE. ISSN: 0017-8748.
DT   Article
LA   English
ED   Entered STN: 2 Jul 1999
       Last Updated on STN: 2 Jul 1999
AB   **Cluster** analysis was used to validate headache diagnostic
       criteria of the International Headache Society (IHS). Structured
       diagnostic interviews were conducted on 443 headache sufferers from a
       community sample, which was randomly split to allow replication.
       Hierarchical cluster analysis of symptoms in both
       subsamples revealed two distinct (P<.001) **clusters**: (1)
       unilateral pulsating pain, pain aggravated by activity, and photophobia
       and phonophobia, and (2) bilateral pressing/tightening pain, mild to
       moderate intensity, and absence of nausea/vomiting. These
       clusters were consistent with IHS migraine and tension-type
       classifications, respectively. Replication using a **non-**

hierarchical clustering technique, k-means **cluster**
analysis, revealed a migrainelike patient **cluster**, reflecting
more frequent pulsating, unilateral pain; more severe pain; and pain
aggravated by activity; nausea, vomiting, photophobia, and phonophobia. A
tensionlike patient **cluster** was also identified, reflecting more
frequent pressing/tightening pain, mild to moderate pain, bilateral
location, and absence of nausea/vomiting. These patient **clusters**
were consistent across subsamples. International Headache Society
diagnoses corresponded with classification based upon statistically
derived **clusters** (P<.001). These results indicate that headache
symptoms **cluster** empirically in a manner consistent with IHS
criteria for migraine and tension-type headaches. Criterion overlap
problems regarding pain intensity and duration were identified. Overall,
these data support migraine and tension-type headache as distinct
entities, and provide support for the IHS diagnostic criteria with minor
modifications.

L6   ANSWER 7 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:238053 BIOSIS
DN   PREV199900238053
TI   Classification and receptor modeling of wet precipitation data from
      Central Austria (1984-1993).
AU   Simeonov, V. [Reprint author]; Puxbaum, H.; Tsakovski, S.; Sarbu, C.;
      Kalina, M.
CS   Faculty of Chemistry, University of Sofia 'St. Kliment Okhridski', J.
      Bourchier Blvd. 1, 1126, Sofia, Bulgaria
SO   Environmetrics, (March-April, 1999) Vol. 10, No. 2, pp. 137-152. print.
      ISSN: 1180-4009.
DT   Article
LA   English
ED   Entered STN: 17 Jun 1999
      Last Updated on STN: 17 Jun 1999
AB   Various classification procedures (**hierarchical** and **non
      -hierarchical** crisp and fuzzy clustering, cross-classification
      fuzzy clustering) and principal component analysis (varimax rotation)
      combined with receptor modeling are applied to a data set consisting of
      wet deposition loads of major ions from five sampling sites in Central
      Austria collected in a period of 10 years (1984-1993). The data
      classification with respect to the sampling sites as objects has shown
      that a distinct separation between sites located at the northern Alpine
      rim (Reutte, Kufstein and Haunsberg) and in the inner Alpine region
      (Innervillgraten and Werfenweng) is achieved indicating in this way the
      role of the geographical disposition of the sampling sites. Both
      cluster and principal components analysis proved that three
      conditional (latent) factors are responsible for the data structure called
      in this study 'anthropogenic', 'crustal' and 'mixed salt' - (NH4+, SO42-,
      NO3-, H+), (Ca2+, Mg2+), (K+, Na+, Cl-), respectively. The source
      apportioning model has indicated that anthropogenic gaseous emissions
      might be responsible for the first factor, natural crustal influences and
      Sahara events for the second and sea salt and manure for the third.

L6   ANSWER 8 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:47046 BIOSIS
DN   PREV199900047046
TI   Genetic diversity in a large collection of wheats (Triticum spp.).
AU   Sharma, P. K.; Gupta, P. K.; Balyan, H. S.

AB   Three hundred genotypes of bread and durum wheats including Indian and exotic collections were evaluated for 10 yield and other related characters. Five characters (grain and biological yields, tiller number, grain weight/ear and grains/ear) exhibited high variability. Of the remaining five traits, flag leaf area and 100-grain weight showed moderate variability while plant height, peduncle length and harvest index showed relatively low variability. Following the **non-hierarchical** euclidean **cluster** analysis, all the 300 genotypes were grouped into 16 **clusters** with variable number of genotypes. Genotypes of heterogeneous origin/place of release, and of different ploidy levels (bread and durum wheats) often grouped together in the same **cluster**, suggesting some degree of ancestral relationship between the genotypes. This also suggested a lack of relationship between the genetic diversity and the ploidy level of genotypes. On the basis of the data on genetic divergence and mean performance of yield and other traits, five diverse and superior genotypes, namely MUW 109, CPAN 3064, CPAN 1556, MUW 104, and CPAN 1998 were selected. Each of these genotypes was exceptionally good for one or more characters and was reasonable for other characters relatives to those of the best check varieties. Therefore, these genotypes may be involved in multiple crossing programme to recover transgressive segregates. Further, on the basis of character associations, it is argued that selection of plants with high biological yield coupled with optimum harvest index (50%) should result in progenies with high grain yield potential in wheat.

AB   This paper describes the implementation of multivariate data analysis: NEURODOC applies the axial k-means method for automatic, **non-hierarchical cluster** analysis and a Principal Component Analysis (PCA) for representing the **clusters** on a map. We next introduce Artificial Neural Networks (ANNs) to extend NEURODOC into a neural platform for the **cluster** analysis and cartography of bibliographic data. The ANNs tested are: the Adaptive Resonance Theory (ART 1), a Multilayer Perceptron (MLP), and an associative network with

unsupervised learning (KOHONEN). This platform is intended for quantitative analysis of information.

AN   1997:339158 BIOSIS
DN   PREV199799638361
TI   The analysis of large scale data taken from the world groundnut (Arachis hypogaea L.) germplasm collection: I. Two-way quantitative data.
AU   Harch, B. D. [Reprint author]; Basford, K. E.; Delacy, I. H.; Lawrence, P. K.
CS   CSIRO, Math. Inf. Sci., PMB 2, Glen Osmond, SA 5064, Australia
SO   Euphytica, (1997) Vol. 95, No. 1, pp. 27-38.
      CODEN: EUPHAA. ISSN: 0014-2336.
DT   Article
LA   English
ED   Entered STN: 11 Aug 1997
      Last Updated on STN: 11 Aug 1997

AB   Data associated with germplasm collections are typically large and multivariate with a considerable number of descriptors measured on each of many accessions. Pattern analysis methods of clustering and ordination have been identified as techniques for statistically evaluating the available diversity in germplasm data. While used in many studies, the approaches have not dealt explicitly with the computational consequences of large data sets (i.e. greater than 5000 accessions). To consider the application of these techniques to germplasm evaluation data, 11328 accessions of groundnut (Arachis hypogaea L) from the International Research Institute for the Semi-Arid Tropics, Andhra Pradesh, India were examined. Data for nine quantitative descriptors measured in the rainy and post-rainy growing seasons were used. The ordination technique of principal component analysis was used to reduce the dimensionality of the germplasm data. The identification of phenotypically similar groups of accessions within large scale data via the computationally intensive **hierarchical** clustering techniques was not feasible and **non-hierarchical** techniques had to be used. Finite mixture models that maximise the likelihood of an accession belonging to a **cluster** were used to **cluster** the accessions in this collection. The patterns of response for the different growing seasons were found to be highly correlated. However, in relating the results to passport and other characterisation and evaluation descriptors, the observed patterns did not appear to be related to taxonomy or any other well known characteristics of groundnut.

AN   1997:217318 BIOSIS
DN   PREV199799523822
TI   Components of relative growth rate and their interrelations in 59 temperate plant species.
AU   Hunt, Roderick [Reprint author]; Cornelissen, J. H. C.
CS   NERC Unit Comparative Plant Ecol., Dep. Animal Plant Sci., Univ. Sheffield, Sheffield S10 2TN, UK
SO   New Phytologist, (1997) Vol. 135, No. 3, pp. 395-417.
      CODEN: NEPHAV. ISSN: 0028-646X.
DT   Article
LA   English
ED   Entered STN: 22 May 1997
      Last Updated on STN: 22 May 1997

AB   Three groups of species (21 herbaceous monocotyledons, 22 herbaceous
     dicotyledons and 16 woody dicotyledons), including representatives of a
     wide range of natural habitats and life forms in inland Britain, were
     grown in the seedling phase in a resource-rich controlled environment and
     assessed over a 14-day period (21 d in the case of woody species). Mean
     values of relative growth rate (RGR), unit leaf rate (ULR), leaf area
     ratio (LAR), leaf weight fraction (LWF), specific leaf area (SLA), and the
     root-shoot allometric coefficient were derived. In herbaceous species,
     the grand mean RGR was 0.20 d-1, comparable to values previously recorded.
     For woody species, the mean was 0.09 d-1. An existing assumption linking
     high RGR to high allocation to photosynthetic biomass was upheld by
     comparisons made between groups. Within groups, however, no pattern of
     this kind could be demonstrated. When photosynthetically active radiation
     was increased from 125 to 250 mu-mol m-2 s-1, ULR was increased almost pro
     rata. The parallel response in RGR was only slight, being offset by
     considerable reductions in LAR. The apparent mean quantum yield for
     photosynthesis in herbaceous species (whole-plant d. wt basis) was 0.60 g
     mol-1. There was no significant dependence of RGR on ULR in any of the
     three groups of species, although the absolute magnitude of ULR declined
     in the order: herbaceous monocotyledons gt herbaceous dicotyledons gt
     woody dicotyledons. In all three groups, RGR was strongly dependent upon
     LAR but no differences emerged in absolute scale of LAR. The absolute
     scale of mean LWF decreased from herbaceous to woody species, but the
     dependence of LAR on LWF strengthened. Groups showed no systematic
     differences in magnitude Of SLA, but the correlation of LAR with SLA was
     strong throughout. Multiple regression showed that the leading
     determinants of RGR were ULR and SLA in herbaceous species and LWF in
     woody species. Principal components analyses (PCA) on each of the three
     groups explained at least 77% of variation and agreed closely with an
     optimal (**non-hierarchical**) classification. Only six
     cluster 'types' were recognized out of the 16 theoretically
     possible combinations of 'high' or 'low' values of the four growth
     parameters. Strong evidence of evolutionary trade-offs emerged, most
     strikingly in that high RGR was never seen in combination with low SLA.
     The morphological/physiological types identified by an all-groups PCA
     separated woody from the herbaceous species, but dicotyledons were almost
     congruent with the monocotyledons. The non-growth-analytical attributes
     most strongly correlated with mean RGR were percentage yield at a low
     level of mineral nutrients, leaf nitrogen concentration, and seed weight.
     It was concluded that mean RGR plays a central role in the identification
     of pathways of evolutionary specialization in herbaceous species.

Last Updated on STN: 12 May 1997
AB   The nature and magnitude of genetic diversity was assessed using
      non-hierarchical euclidean **cluster** analysis in
      405 pure breeding lines of T. aestivum for grain yield and its associated
      traits. All the genotypes got grouped in 13 different **clusters.**
      The clustering pattern of the genotypes belonging to the same country
      revealed their distribution in more than one **cluster** showing
      nonparallelism between geographic and genetic diversity. Members of
      cluster IV and IX were highly diverse from each other.
      Cluster VI had high mean values for grain yield, biological yield,
      number of tillers/unit area and harvest index. A number of genotypes were
      also identified which may serve as potent genetic donors for some metric
      traits.

L6   ANSWER 13 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:573845 BIOSIS
DN   PREV199799288526
TI   Floristic patterns and phytogeography of Skane, S Sweden.
AU   Andersson, Per-Arne [Reprint author]; Weimarck, Gunnar
CS   Dep. Ecological Botany, Villavagen 14, S-752 36 Uppsala, Sweden
SO   Acta Universitatis Upsaliensis Symbolae Botanicae Upsalienses, (1996) Vol.
      31, No. 3, pp. 239-264.
      CODEN: SBUPAC. ISSN: 0082-0644.
DT   Article
LA   English
ED   Entered STN: 23 Dec 1996
      Last Updated on STN: 23 Dec 1996
AB   Dot maps of the distribution of 895 vascular plant taxa in the province of
      Skane, S Sweden, were digitized and the records assigned to 483 quadrats
      of 5 times 5 km each. Quadrats and species were classified by the
      non-hierarchical agglomerative clustering program TABORD
      and ordinated by the program DECORANA. The results are given in a
      phytosociological table and as grid map plots and ordination graphs.
      Gradients are interpreted and **clusters** described in terms of
      Ellenberg's indicator scores. A regional floristic subdivision of the
      province in eight areas is proposed. The position of the border, 'limes
      scanicus', between two previously proposed major areas is modified here.

L6   ANSWER 14 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:283806 BIOSIS
DN   PREV199699006162
TI   Genetic divergence in greengram (Phaseolus radiatus) germplasm through use
      of **non-hierarchical** Euclidean **cluster**
      analysis.
AU   Sharma, B. L. [Reprint author]; Singh, D. P.; Ram, H. H.
CS   Dep. Genetics Plant Breeding, Pantnagar, Uttar Pradesh 263 145, India
SO   Indian Journal of Agricultural Sciences, (1996) Vol. 66, No. 3, pp.
      193-196.
      CODEN: IJASA3. ISSN: 0019-5022.
DT   Article
LA   English
ED   Entered STN: 25 Jun 1996
      Last Updated on STN: 25 Jun 1996

L6   ANSWER 15 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:238517 BIOSIS

TI   Comparative anatomy of the wood of Quercus affinis and Q. laurina
      (Fagaceae).
AU   Valencia Avalos, Susana [Reprint author]; Barajas-Morales, Josefina
CS   Herbario FCME, Fac. Ciencias, UNAM, Apdo. Postal 70-399, Del. Coyacan,
      04510 Mexico, D.F., Mexico
SO   Anales del Instituto de Biologia Universidad Nacional Autonoma de Mexico
      Serie Botanica, (1995) Vol. 66, No. 2, pp. 113-131.
      CODEN: AMXSAH. ISSN: 0374-5511.
DT   Article
LA   Spanish
ED   Entered STN: 28 May 1996
      Last Updated on STN: 28 May 1996
AB   Quercus affinis Scheidweiler and Quercus laurina Humboldt et Bonpland, are
      morphologically very similar making their identification very difficult.
      Their wood anatomy was studied in order to use it as an aid in a more
      precise identification. The anatomical qualitative and quantitative
      characteristics of the wood of both species were compared, using the data
      of Q. acherdophylla as a standard reference. The macroscopic and
      microscopic data were compared using **non hierarchical**
      statistics tests of discriminant analysis and by the technique of
      cluster average league (UPGMA). The results confirm the existence
      of two well differentiated taxa, Q. affinis and Q. laurina, and an
      intermediate group that we are calling Q. affinis times Q. laurina from
      the neovolcanic axis. The anatomical traits more useful in delimiting
      taxa are porosity type, growth rings, sapwood color, grain type, fiber
      length, vessel diameter, and width of multiseriate rays.

L6   ANSWER 16 OF 33   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:21659 BIOSIS
DN   PREV199698593794
TI   Genetic diversity in South Asian okra (Abelmoschus esculentus) germplasm
      collection.
AU   Bisht, I. S.; Mahajan, R. K.; Rana, R. S.
CS   Natl. Bureau Plant Genetic Resources, Pusa Campus, New Delhi 110012, India
SO   Annals of Applied Biology, (1995) Vol. 126, No. 3, pp. 539-550.
      CODEN: AABIAV. ISSN: 0003-4746.
DT   Article
LA   English
ED   Entered STN: 12 Jan 1996
      Last Updated on STN: 12 Jan 1996
AB   Genetic diversity for a range of morphological characters within 260
      accessions of okra collected from India, Bangladesh, Nepal and Sri Lanka
      was investigated through the use of uni-, bi- and multivariate statistics.
      The pubescence and pigmentation of various plant parts, among qualitative
      descriptors, seemed to be most significant in the analysis of variability.
      The multivariate analysis, mainly on quantitative descriptors, using
      principal component and **non-hierarchical**
      cluster analysis suggested that days to flowering, plant height,
      and various fruit characteristics were important components of variability
      and contributed significantly to the total variation observed. Only two
      of the 10 principal components had eigen values more than 1 and together
      accounted for 54.52% of the total variation. The accessions were grouped
      into eight distinct **clusters** which further emphasized the
      relative contribution of various quantitative characters to the total
      variability. The pattern of genetic variation is of great importance both

to germplasm collectors and plant breeders. Specific accessions were also identified that could be passed on to breeders for utilization in crop improvement programme.

L6   ANSWER 17 OF 33   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1994:526576   BIOSIS
DN   PREV199497539576
TI   Computer-assisted mapping of paddy-field soils: II. Classification, mapping and significance.
AU   Ishida, Tomoyuki [Reprint author]; Ando, Ho
CS   Fac. Agric., Kagawa Univ., Kida-gun, Kagawa 761-07, Japan
SO   Soil Science and Plant Nutrition, (1994) Vol. 40, No. 3, pp. 403-414.
      CODEN: SSPNAW. ISSN: 0038-0768.
DT   Article
LA   English
ED   Entered STN: 15 Dec 1994
      Last Updated on STN: 16 Dec 1994
AB   In order to determine how a conventional soil map on a local scale can be reproduced from soil sample information, a set of numerical procedures was applied to the soil chemical data from 159 soil samples collected in paddy fields of the Aizu Basin, in the northern part of Japan. The digital elevation data were also included as an attribute. Various steps were involved. In the first step, the sparse data were converted into a closely spaced data set. This first step was previously described in Part I of this paper. In the second step a multivariate ordination (principal component analysis) was applied to the sampling data in order to avoid redundancy of information. Large contributions to the first component were derived from the values of CEC and exchangeable Ca and Mg. In the third step the sampling sites were numerically classified using the results of four or five components obtained in the second step. A **hierarchical** clustering method was applied to provide the initial set of **clusters** for **non-hierarchical** clustering. In the fourth step the closely spaced data collected in the first step were allocated to an appropriate class obtained by using the **non-hierarchical** clustering method applied in the third step. For the allocation method, the geographic location of the sampling sites was included as an additional characteristic of the data. In the regional partition map based on the numerical procedures, each soil group corresponded to a soil series in the original conventional soil map which depended predominantly on detailed morphological and topographical differences. In addition, the regional partition map was found to provide useful information for the identification of factors closely related to soil fertility, by statistically examining the differences in rice yield among the soil groups.

L6   ANSWER 18 OF 33   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1994:346196   BIOSIS
DN   PREV199497359196
TI   The effects of osmotic pre-sowing treatment on laboratory germination in a range of wild flower species.
AU   Tallowin, J. R. B.; Rook, A. J.; Brookman, S. K. E.
CS   AFRC Inst. Grassland and Environmental Res., North Wyke Res. Station, Okehampton, Devon, EX20 2SB, UK
SO   Annals of Applied Biology, (1994) Vol. 124, No. 2, pp. 363-370.
      CODEN: AABIAV. ISSN: 0003-4746.
DT   Article

LA   English
ED   Entered STN: 8 Aug 1994
        Last Updated on STN: 8 Aug 1994

AB   Sown seed of many wild flower species have slow or delayed germination
        which can allow unsown and undesirable species to colonize a prepared
        site. Ideally all seed sown should germinate immediately. Priming seed
        in an inert osmoticum can improve synchronization and speed of
        germination. The objective of this study was to assess the efficacy of
        priming on a selection of 60 wild flower species from a total of 21
        different families. The majority of the species selected were common
        constituents of commercial seed mixtures. Seeds were primed in the light
        at 15 degree C for 14 days in a polyethylene glycol '6000' solution giving
        an osmotic potential of either -10 or -15 bars. Priming had a highly
        significant effect on speed of germination reducing the median germination
        time by 2.8 +- 0.27 days in the -10 bar treatment and 1.6 +- 0.27 days in
        the -15 bar treatment. At the species level, 28 species had significantly
        reduced median germination times following priming. Priming significantly
        enhanced the final germination percentage in 15 species and significantly
        reduced it in eight species, with the adverse effect being more pronounced
        at -15 bars than at -10 bars. **Non-hierarchical
        cluster** analysis showed no clear patterns in response to priming
        either in relation to the comparative ecology or the plant family of the
        species tested, with the possible exception of the Leguminosae species.
        Only one out of six members of this family showed any enhancement in
        germination rate or percentage. The study demonstrates that a priming
        treatment could improve speed of germination. in a wide range of commonly
        sown semi-natural grassland species.

AN   1994:345339 BIOSIS
DN   PREV199497358339
TI   Application of multivariate analysis to site quality evaluation for
        coniferous plantations.
AU   Ares, Adrian
CS   Dep. Agronomy Soil Sci., Univ. Hawaii at Manoa, 1910 East-West Road,
        Honolulu, HI 96822, USA
SO   South African Forestry Journal, (1993) Vol. 0, No. 167, pp. 27-34.
        CODEN: SAFJBF. ISSN: 0038-2167.
DT   Article
LA   English
ED   Entered STN: 8 Aug 1994
        Last Updated on STN: 8 Aug 1994

AB   Multivariate analysis was performed on tree growth and environmental data
        from sites afforested with conifers in Ventania, southern Buenos Aires,
        Argentina. Pinus halepensis was investigated in 22 sites, Pinus radiata
        in 20 sites and Cedrus deodara and Cupressus sempervirens f. horizontalis
        in 15 sites each. Site index expressed as height of dominants at age 25
        years was used as growth indicator. Four site quality classes were set up
        for each of the four species. Twenty three topographic and soil
        characteristics were used to group the sites into six groups by means of a
        non-hierarchical cluster analysis technique.
        The groups were then used to test the ability of the environmental
        variables to discriminate among site quality classes. Standardised mean
        site index of stands on cumulic soils were significantly higher than those
        on shallow soils. A **hierarchical** technique used to establish
        intergroup relationships produced similar results to **cluster**

analysis. Seven variables were selected as potential discriminators
between growth response groups for all the species studied. Only rooting
depth and depth to C horizon, rock or calcium carbonate layer, were
finally selected as discriminators. It is concluded that rooting depth
should be used as primary discriminant among sites in land evaluation for
forestry in the region.

L6   ANSWER 20 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:386396 BIOSIS
DN   PREV199396061696
TI   Comparing three classification strategies for use in ecology.
AU   Belbin, Lee [Reprint author]; McDonald, Cam
CS   CSIRO Div. Wildlife and Ecol., PO Box 84, Lyneham, ACT Australia 2602,
      australia
SO   Journal of Vegetation Science, (1993) Vol. 4, No. 3, pp. 341-348.
      CODEN: JVESEK. ISSN: 1100-9233.
DT   Article
LA   English
ED   Entered STN: 23 Aug 1993
      Last Updated on STN: 23 Aug 1993
AB   We compare three common types of clustering algorithms for use with
      community data. TWINSPAN is divisive **hierarchical**,
      flexible-UPGMA is agglomerative and **hierarchical**, and ALOC is
      non-hierarchical. A balanced design six-factor model
      was used to generate 480 data sets of known characteristics. Recovery of
      the embedded **clusters** suggests that both flexible UPGMA and ALOC
      are significantly better than TWINSPAN. No significant difference existed
      between flexible UPGMA and ALOC.

L6   ANSWER 21 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1992:285821 BIOSIS
DN   PREV199294010471; BA94:10471
TI   ELECTRON MICROPROBE CHARACTERIZATION OF INDIVIDUAL AEROSOL PARTICLES
      COLLECTED BY AIRCRAFT ABOVE THE SOUTHERN BIGHT OF THE NORTH SEA.
AU   ROJAS C M [Reprint author]; VAN GRIEKEN R E
CS   DEP CHEM, UNIV ANTWERP, UNIVERSITEITSPLEIN 1, B-2610 ANTWERP-WILRIJK,
      BELGIUM
SO   Atmospheric Environment Part A General Topics, (1992) Vol. 26, No. 7, pp.
      1231-1237.
      CODEN: AEATEN. ISSN: 0960-1686.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 10 Jun 1992
      Last Updated on STN: 10 Jun 1992
AB   About 50,000 individual aerosol particles from a total of 108 samples
      collected at six different altitudes above the Southern Bight of the North
      Sea, have been analyzed using electron probe X-ray microanalysis. The
      results of **hierarchical cluster** analysis on each
      sample revealed that, for continental air masses, most of the aerosol
      particulate matter is characterized by high amounts of aluminosilicates,
      CaSO4 and Fe-rich particles. For western and marine air masses there was
      no change in the composition of the most abundant particle type with
      height. This is in connection with the rather mixed nature of the
      atmosphere. **Non-hierarchical cluster**
      analysis showed that the most abundant particle types in this airshed are:

aluminosilicates from coal combustion releases, Fe-rich, sea salts
enriched with Pb, and organic material associated with residual oil
combustion tracers, accounting for 21, 16, 15 and 12% of the total
analyzed particles, respectively. Almost 60% of the analyzed particles is
related to combustion or energy-generation processes. Principal factor
analysis on an elemental frequency matrix led to comparable results with
principal factor analysis used in combination with **cluster**
analysis. This shows that the method described here is useful for the
identification of aerosol sources.

L6   ANSWER 22 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1992:53871 BIOSIS
DN   PREV199293033846; BA93:33846
TI   AN EMPIRICAL EVALUATION OF THE MBTI TYPOLOGY.
AU   LORR M [Reprint author]
CS   LIFE CYCLE INSTITUTE, THE CATHOLIC UNIV OF AMERICA, WASHINGTON, DC 20064,
      USA
SO   Personality and Individual Differences, (1991) Vol. 12, No. 11, pp.
      1141-1146.
      ISSN: 0191-8869.
DT   Article
FS   BA
LA   .ENGLISH
ED   Entered STN: 13 Jan 1992
      Last Updated on STN: 13 Jan 1992
AB   The popular Myers-Briggs Type Indicator (MBTI) applies a classification
      schema that allocates all respondents to one of 16 types on the basis of
      four preference scores. The study's aim was to evaluate the empirical
      validity of the MBTI classification scheme. The approach taken was to
      apply two **cluster** analytic procedures to the four standardized
      scale scores. One method applied was Ward's **hierarchical**
      grouping procedure and the other a **non-hierarchical**
      average linkage. Five **clusters** in the first sample of 100 men
      could be matched across the two procedures, and four **clusters** in
      the second sample of 100 were also matched. On the whole, agreement
      between the MBTI 16 categories and the empirically derived
      clusters was weak or negligible. Some reasons why the MBTI
      typology is defective as a classification scheme are carefully delineated.

L6   ANSWER 23 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1990:376848 BIOSIS
DN   PREV199090063529; BA90:63529
TI   ALLOMETRY IN LITHODES-ANTARCTICUS JACQUINOT 1983 CRUSTACEA DECAPODA LENGTH
      OF THE RIGHT CHELA VERSUS CARAPACE LENGTH.
AU   GUZMAN-M L [Reprint author]; RIOS-C C
CS   AREA DE BIOL, INST DE LA PATAGONIA, UNIV DE MAGALLANES, CASILLA 113-D,
      PUNTA ARENAS, CHILE
SO   Anales del Instituto de la Patagonia Serie Ciencias Naturales, (1987) Vol.
      17, pp. 89-98.
      ISSN: 0716-6486.
DT   Article
FS   BA
LA   SPANISH
ED   Entered STN: 21 Aug 1990
      Last Updated on STN: 21 Aug 1990
AB   Right chela length and carapace length relationship in males of Lithodes

antarcticus Jacquinot 1853, from five fishing areas of the Magellan region
(between 50° and 54° 30' S.L.) was studied. Specimens were
collected approximately up to 60 m depth, between September-October 1980
and January-February 1984. Information was analyzed using a regression
analysis applying the linearized allometric growth equation. Data from
juveniles (inmatures) and adults (matures) were studied separately. Due
to individual variability, there is a size range, where inmature and
mature specimens overlap. Specimens from this range were classified
according to a morphometric criterion, using a technique similar to a
non hierarchical cluster analysis. Relative
growth between both body structures is isometric in the juvenile phase,
and allometric during the adult phase. This growth pattern is associated
to sexual maturity, being the chela length increase about 15% higher
during the adult phase. Juveniles from the five study areas showed a
homogenous relative growth rate, and a similar results was obtained for
adults. Thus, a common regression for each growth phase was calculated.
Differences between studied stocks are in the sizes at which occur the
rupture of growth line. The size range of this rupture in each sector is
defined by the sizes of the "smallest mature specimen" and the "largest
inmature specimen". There is a high overlap of this size range between
study sectors, difficulting, specimens identification to precise capture
area if right chela size is used. More studies are needed to comprise
geographic morphometric variations and to detect evolutive divergence
features in relative growth of L. antarcticus stocks in the Magellan
region.

L6   ANSWER 24 OF 33   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1990:223971   BIOSIS
DN   PREV199089121261; BA89:121261
TI   MULTIVARIATE APPROACH TO GROUPING SOILS IN SMALL FIELDS II. SOIL GROUPING
        TECHNIQUE BY **CLUSTER** ANALYSIS.
AU   KOSAKI T [Reprint author]; JUO A S R
CS   DEP AGRO-ENVIRON SCI, OBIHIRO UNIV AGRIC VETERINARY MED, OBIHIRO 080, JPN
SO   Soil Science and Plant Nutrition, (1989) Vol. 35, No. 4, pp. 517-526.
        CODEN: SSPNAW. ISSN: 0038-0768.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 10 May 1990
        Last Updated on STN: 10 May 1990
AB   **Cluster** analysis was applied in grouping soils based on their
        scores of the factors controlling soil variation in a cultivated, field at
        the Experimental Farm of the International Institue of Tropical
        Agriculture in Ibadan, Nigeria. The procedure employed here consisted of
        two steps: 1) grouping of the samples into a given number of provisional
        clusters through **non-hierarchical**
        cluster analysis, and 2) analysis of the similarity among those
        clusters using their means with **hierarchical**
        cluster analysis and determination of the proper number of the
        final **clusters.** Two initial settings in the assignment of the
        number of the provisional **clusters** were tested in **non-**
        hierarchical cluster analysis. Both trials gave a
        consistent classification, which also agreed with that based only on
        hierarchical cluster analysis. This combination of
        non-hierarchical and **hierarchical**
        cluster analsyses enabled us to pressure a soil map solely based

on the factors controlling soil variation in the study area without
introducing an a priori idea of soil classification. This method is not
only an alternative to **hierarchical** clustering, but a more
efficient tool in terms of capacity and computational speed to classify
large numbers of samples which **hierarchical cluster**
analysis is unable to handle.   .

L6   ANSWER 25 OF 33   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1989:355631   BIOSIS
DN   PREV198988047745; BA88:47745
TI   MIDWATER FOOD WEB IN THE VICINITY OF A MARGINAL ICE ZONE IN THE WESTERN
        WEDDELL SEA ANTARCTIC.
AU   HOPKINS T L [Reprint author]; TORRES J J
CS   DEP MARINE SCI, UNIV SOUTH FLORIDA, 140 7TH AVE SOUTH, ST PETERSBURG, FLA
        33701, USA
SO   Deep-Sea Research Part A Oceanographic Research Papers, (1989) Vol. 36,
        No. 4, pp. 543-560.
        CODEN: DRPPD5. ISSN: 0198-0149.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 2 Aug 1989
        Last Updated on STN: 2 Aug 1989
AB   The structure of the food web in the vicinity of a marginal ice zone was
        investigated in the western Weddell Sea during austral autumn 1986. The
        diets of 40 species of zooplankton and micronekton occurring in the
        epipelagic zone were examined and compared using **non-
        hierarchical** clustering procedures. Over half the species were in
        three **clusters** of predominately small-particle (phytoplankton;
        protozoans) grazers. These included biomass dominants Calanoides acutus,
        Calanus propinquus, Metridia gerlachei and Salpa thompsoni. Six
        clusters contained omnivores that had diets consisting of small
        particles as well as a substantial fraction of metazoan food. Among these
        was Euphausia superba. Seven groups were carnivorous, including species
        of copepods (1), chaetognaths (3), and fishes (5). Copepods were the most
        frequent food of carnivores; however krill also were important in the
        diets of three fish species. Among small-particle grazers, phytoplankton
        occurred more frequently in guts in individuals from open water; carnivory
        was more in evidence in samples collected under the pack ice. Regional
        comparisons of material taken on this and several previous cruises
        indicate that, in most of the dominant species, diets remain relatively
        consistent with respect to major food categories. Seasonal impact on
        feeding dynamics appears to be great: the guts of grazing species were
        generally much more full (visual evidence) during summer bloom conditions
        than during the autumn. The following trophic sequence is suggested for
        grazing zooplankton species in ice-covered regions of the Antarctic: (1)
        Active small-particle grazing during the summer bloom period; (2) reduced
        ingestion rates in autumn as primary production declines and the system
        becomes more oligotrophic, with some species augmenting grazing with
        carnivory; (3) descent of zooplankton biomass species into the mesopelagic
        zone in late autumn-early winter with feeding largely terminated. The
        sequence applies to the dominant zooplankton biomass species. Feeding
        dynamics and vertical distribution of several of the important larger
        sized grazing species, such as Euphausia superba and Salpa thompsoni,
        remain largely unknown.

AN   1989:294212 BIOSIS
DN   PREV198988019556; BA88:19556
TI   EVALUATION OF LOCAL COLLECTIONS OF WHEAT TRITICUM-SPP GERMPLASM.
AU   GARG D K [Reprint author]; GAUTAM P L
CS   DEP AGRIC BOTANY, INST ADVANCED STUDIES, MEERUT UNIV, MEERUT-250005, UP,
      INDIA
SO   Genetica Agraria, (1988) Vol. 42, No. 3, pp. 255-262.
      CODEN: GEAGAC. ISSN: 0016-6685.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 20 Jun 1989
      Last Updated on STN: 20 Jun 1989
AB   **Non-Hierarchical** Euclidean **cluster** analysis
      was used as a measure of genetic divergence among 377 Indian local wheat
      collections. Fifteen yield and yield contributing characters were used.
      All the collections were grouped into 15 different **clusters**
      showing the existence of high genetic diversity. **Cluster** 12 had
      the genotypes of high mean value for grain yield per plant.
      Shannon-Weaver diversity index (H') was used for working out genetic
      diversity among morphological characters. Maximum morphological variation
      (H' = 1.35) was observed in the collections from the hills of Uttar
      Pradesh (India). The germplasm collections with reasonable degree of
      resistance to rusts and powdery mildew were also identified.

AN   1986:358846 BIOSIS
DN   PREV198682063320; BA82:63320
TI   **NON-HIERARCHICAL** EUCLIDEAN **CLUSTER** ANALYSIS
      IN CELERY.
AU   SETHI K L [Reprint author]; SAPRA R L
CS   NATL BUREAU PLANT GENETIC RESOURCES, NEW DELHI
SO   International Journal of Tropical Agriculture, (1986) Vol. 4, No. 1, pp.
      73-76.
      CODEN: IJTADD. ISSN: 0254-8755.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 6 Sep 1986
      Last Updated on STN: 6 Sep 1986
AB   Genetic diversity studies were carried out and in celery the germplasm
      classification subjected to '**Non-Hierarchical**
      Euclidean **Cluster** Analysis' taking into consideration the
      variation explained by all the eigen roots using the method of Beale
      (1969). The percentage of variation explained with the help of two eigen
      roots was only 64.66 per cent and not sufficient to follow the graphical
      approach in two dimensional spaces.

AN   1986:150785 BIOSIS
DN   PREV198681061201; BA81:61201
TI   FOOD WEB OF AN ANTARCTIC MIDWATER ECOSYSTEM.
AU   HOPKINS T L [Reprint author]
CS   DEP MARINE SCI, UNIV SOUTH FLA, ST PETERSBURG, FL 33701, USA
SO   Marine Biology (Berlin), (1985) Vol. 89, No. 2, pp. 197-212.

AB   The diets of 93 species of plankton and micronekton taken in the upper
     1000 m of Crocker Passage (Gerlache Strait) in the austral fall, 1983,
     were examined and the principal features of the food web were
     characterized. Most species were small particle feeders, with
     phytoplankton and debris (of phytoplankton and krill) being the principal
     diet components. Krill remains were found in the guts of the majority of
     species examined, with the krill playing a greater role in the form of
     molts and debris than as living prey. Carnivores fed mostly on copepods,
     coelenterates and salps. Some of the larger species fed on live krill.
     Non-hierarchical cluster analysis of diet
     information supported the concept of resource partitioning and determined
     the arrangement of the species into 21 feeding groups. **Cluster**
     analysis groupings tended to be along genetic lines with closely related
     and morphologically similar species having similar diets. These analyses
     were based on collections made in the austral fall (March-April, 1983)
     when phytoplankton standing crop was low, most zooplankton species had
     descended into the mesopelagic zone, and some of the more abundant
     species, such as Calanoides acutus, had ceased feeding. Because the
     trophodynamics of Antarctic ecosystems is strongly pulse-induced, it is
     essential to examine the food web at different periods in the seasonal
     cycle.

AN   1985:240354 BIOSIS
DN   PREV198579020350; BA79:20350
TI   PLANKTONIC COPEPODS IN THE LAGOON OF NEW-CALEDONIA ECOLOGICAL FACTORS AND
     SPECIES ASSEMBLAGES.
AU   BINET D [Reprint author]
CS   ANTENNE ORSTOM, CENTRE OCEANOLOGIQUE DE BRETAGNE, BP 337, F-29273, BREST
     CEDEX, FRANCE
SO   Marine Biology (Berlin), (1984) Vol. 82, No. 2, pp. 143-156.
     CODEN: MBIOAJ. ISSN: 0025-3162.
DT   Article
FS   BA
LA   FRENCH
AB   In the southwestern part of the lagoon of New Caledonia (South Pacific
     Ocean), a plankton sampling program was conducted from Feb. 1978 to April
     1979. During 11 cruises, 5 stations in the open sea and various bays were
     sampled at approximately monthly intervals. A transect of 3 stations
     (mid-lagoon, near-reef and barrier-reef channel), visted every 2 wk,
     completed the sampling program. The 52 most abundant copepod species were
     analyzed for seasonal and regional variations. Cruise and transect data,
     dealt with separately, were analyzed in a variety of ways. Correspondence
     analyses (reciprocal averaging) of qualitative and quantitative copepod
     counts were made. Species partition was achieved by 2 successive methods:
     non-hierarchical, followed by **hierarchical**
     classification. Between-species distance was computed from their
     coordinates on the factorial axis. Species **clusters** obtained
     were plotted in the factorial planes to assess ecological preferences.
     The main ecological factors appear to be spatial patterns, seasonal

temperature cycle, and changes in wind force and direction. Different
populations inhabit the open sea, near-reef, mid-lagoon, shallow and
deep-bay waters. Acartia australis outnumbers all other species in the
reef vicinity. A. amboinensis is the most abundant in the deep,
fjord-like bay. Canthocalanus pauper, Paracalanus parvus, Bestiola sp.,
Centropages orsinii and A. bispinosa are characteristic of shallow bays.
Seasonal barycenters appear close to some station barycenters: summer
close to mid-lagoon, winter close to open sea, and spring close to
near-reef barycenters, respectively. This may be explained by the
seasonal dynamics of the lagoon water. Variations of plankton populations
and biomass in the lagoon seem to be governed by the direction of water
flow across the reef channels. Enrichment factors are terrestrial
sediment wash-out after rainfall and, probably, trade wind-induced
upwelling.

L6   ANSWER 30 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1984:337831 BIOSIS
DN   PREV198478074311; BA78:74311
TI   DISSOLVED OXYGEN CONCENTRATIONS IN LAKE ERIE USA CANADA 1. STUDY OF
      SPATIAL AND TEMPORAL VARIABILITY USING **CLUSTER** AND REGRESSION
      ANALYSIS.
AU   ANDERSON J E [Reprint author]; EL-SHAARAWI A H; ESTERBY S R; UNNY T E
CS   DEP OF CIVIL ENGINEERING, UNIV OF WATERLOO, WATERLOO, ONT N2L 3G1, CANADA
SO   Journal of Hydrology (Amsterdam), (1984) Vol. 72, No. 3-4, pp. 209-230.
      CODEN: JHYDA7. ISSN: 0022-1694.
DT   Article
FS   BA
LA   ENGLISH
AB   A **non-hierarchical** nearest-centroid clustering method
      was used to separate data pairs consisting of the dissolved oxygen (DO)
      concentration and temperature into 4 groups corresponding to hypolimnetic
      and non-hypolimnetic water of the Central and Eastern Basins of Lake Erie.
      For the stations which were common to all cruises within a year and were
      classified as being in the hypolimnion, initial DO concentrations and
      depletion rates were calculated and tests about their constancy were
      performed using weighted regression analysis and regression models with
      the time structure of the data explicitly incoporated in the models. The
      yearly uncorrected depletion rates for 1967-1980 were similar to values
      previously reported by several authors, indicating that this
      semi-objective clustering procedure provides a practical alternative to
      subjective selection of data. The conclusions about constancy of initial
      concentraitons and depletion rates based on an unweighted regression
      analysis were shown to differ from those of weighted regression. Using
      regression with empirical weights, neither the initial DO concentration
      nor the depletion rate remained constant between 1967 and 1980 in the
      Central Basin but the depletion rate remained constant and the initial DO
      concentration varied in the Eastern Basin.

L6   ANSWER 31 OF 33 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1982:149074 BIOSIS
DN   PREV198273009058; BA73:9058
TI   **HIERARCHICAL** CLASSIFICATION OF COMMUNITY DATA.
AU   GAUCH H G JR [Reprint author]; WHITTAKER R H
CS   SECTION OF ECOLOGY SYSTEMATICS, CORNELL UNIV, ITHACA, NEW YORK 14850, USA
SO   Journal of Ecology, (1981) Vol. 69, No. 2, pp. 537-558.
      CODEN: JECOAB. ISSN: 0022-0477.

AB   The application of **hierarchical** classification to ecological
     community data is examined, using a variety of classification techniques
     and test data sets. Problems discussed include the choice of a conceptual
     space in which points representing samples or species or both are located;
     the effects of random noise and nonlinearity; the degree to which
     clusters are natural to a data set or are imposed by the
     clustering technique; the choice of criteria for locating divisions;
     clustering strategies (**non-hierarchical** vs.
     hierarchical, divisive vs. agglomerative and polythetic vs.
     monothetic); the presentation of results of various clustering techniques;
     and methods for evaluating and comparing clustering techniques and their
     results. Five **hierarchical** clustering techniques are compared:
     complete linkage clustering, the unweighted pair group method using
     arithmetic averages, minimization of within-group dispersion, 2-way
     indicator species analysis, and partitioning of an ordination space (using
     detrended correspondence analysis, a modification of reciprocal
     averaging). The first 3 techniques are agglomerative and the last 2 are
     divisive. Data sets for tests include simulated data sets in 1 to 4
     dimensions (some incorporating noise of 3 kinds), and field data varying
     in number of samples, noise level and number and length of community
     gradients. Two-way indicator species analysis is usually the best, but
     there are cases in which other techniques may be complementary or
     superior. Theoretical requirements and test results are discussed to show
     why clustering of ecological community data is usually best approached by
     a divisive strategy. This conclusion is important because the analysis
     may be stopped after a limited number of divisions, thus needing less
     computation than do agglomerative strategies. The 2 divisive techniques
     discussed here have computer requirements which rise only linearly with
     the amount of data, making analysis of large data sets practical.

AB   Structure-seeking techniques were applied to dermatoglyphic variables from
     samples of human populations in the North Pennine Dales, northern England
     [UK], including 1624 males and 1788 females. Results of multivariate
     analyses on 50 palmar variables are included; details on the fingers were
     reported earlier. Previous work disclosed low associations between palm
     and finger variables. The palmar variables include 3 interdigital ridge
     counts, 13 topological patterns, deltas ef, t, t', t" and tb and the 4
     mainlines A, B, C and D for each hand. Two ordinal coding schemes were
     used for the mainlines in order to process blind terminations of the
     proximal radiants. A nascent scheme treats blind terminations of lines as

embryonic and of low rank; a sequential scheme interprets them as acute
reflections of the proximal radiants to source, attributing to them a
correspondingly higher rank. Analyses have been effected by way of
non-metric scaling algorithms and factoring techniques on ordinal
connection matrices for each sex. Solutions are displayed as non-metric
2-dimensional scaling plots of the variables on which are superimposed
non-hierarchical partially overlapping **clusters**
of varimax rotated factors. Results are in agreement for nascent and
sequential coding schemes depicting 11 non-overlapping and 3 overlapping
clusters. The latter comprise interdigital variables, namely
lines B, C and D, patterns III, IIIT and IV and ridge count bc.
Subsequent ordination revealed consistent relationships in this group,
clear variable homolog linkages and distinct bilateral **clusters**;
and a distinctly less compact assortment of left hand as opposed to right
hand variables.

L6   ANSWER 33 OF 33   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1980:183429   BIOSIS
DN   PREV198069058425; BA69:58425
TI   DISTRIBUTION OF WESTERN BEAUFORT SEA ALASKA USA POLYCHAETOUS ANNELIDS.
AU   BILYARD G R [Reprint author]; CAREY A G JR
CS   SCH OCEANOGR, OREG STATE UNIV, CORVALLIS, OREG 97331, USA
SO   Marine Biology (Berlin), (1979) Vol. 54, No. 4, pp. 329-340.
      CODEN: MBIOAJ. ISSN: 0025-3162.
DT   Article
FS   BA
LA   ENGLISH
AB   Depth and depth-related processes appear to exert primary control over the
      distributional patterns of species of polychaetous annelids in the western
      Beaufort Sea (Cape Halkett-Barter Island, Alaska). Species richness and
      total polychaete abundance are maximal along the outer continental shelf
      and upper continental slope. Stations exhibiting the most similar
      polychaete assemblages are located at similar depths. Some species
      distributions appear to correlate better with sediment type than with
      depth. Maximum abundance occurs deeper on the continental slope to the
      west; and station **clusters** generated by **non-**
      hierarchical clustering (using the dominant polychaete species
      data) are not sorted strictly by depth. In a canonical analysis of
      discriminance, the station **clusters** were projected onto a 2
      dimensional plane in species space. The 1st and 2nd canonical variables
      of the station **clusters** correlate with sediment grain-size
      distributions, suggesting a relationship between polychaete distribution
      patterns and the sedimentary environment. This relationship is further
      substantiated when sediment grain-size distributions for each station are
      plotted on a tertiary diagram: the stations are grouped and ordered in a
      pattern similar to that generated by the canonical analysis of
      discriminance.

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☐	L2	L1 same cluster$	67
☐	L1	hierarchical same non-hierarchical	988

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